



STIC Search Report

Biotech-Chem Library

29

STIC Database Tracking Number: 165851

TO: Minh-Tam Davis
Location: rem/3A24/3C18
Art Unit: 1642
Thursday, April 20, 2006
Case Serial Number: 09/762577

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: (571)272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Davis,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2523

pnorty 08/98

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736 22

M3

STIC-Biotech/ChemLib

185851

From: Chan, Christina
Sent: Tuesday, April 18, 2006 11:26 AM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/762577

Please rush Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644

(571)-272-0841

Remsen, 3E89

-----Original Message-----

From: Davis, Minh-Tam
Sent: Monday, April 17, 2006 4:57 PM
To: Chan, Christina
Subject: Rush search request for 09/762577

Please search in commercial database, issued patent files, PGPUB and interference:

- 1) SEQ ID NO:11.
- 2) The nucleic acid encoding SEQ ID NO:12.

Thank lyou.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

272-0830

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Db 273 TCTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 332
QY 319 CAGATCTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 378
Db 333 CAGATCTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 392
QY 379 ACCTTGTCTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 438
Db 393 ACCTTGTCTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 452
QY 439 TTCTATGACTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 498
Db 453 TTCTATGACTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 512
QY 499 TTCCACACAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 558
Db 513 TTCCACACAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 572
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Db 573 TGGAGAGGCGGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 632
QY 619 CTGCTCCGCTCAAAAGAGAGACTTGTCTCAAGTGTGAGAGACTCACTCCAGCTG 678
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QY 1159 AGGAGGCGGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 1218
Db 1173 AGGAGGCGGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 1232
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RESULT 2
US-09-127-928-1
; Sequence 1, Application us/09127928
; Patent No. 6472172
; GENERAL INFORMATION:
; APPLICANT: Deng, Gang

APPLICANT: Lin, Jiling-Huey
APPLICANT: Morse, Michael J
TITLE OF INVENTION: DNA Encoding a No. 6472172el Human Inhibitor-of-Apoptosis
FILE REFERENCE: Protein
CURRENT APPLICATION NUMBER: US/09/127,928
CURRENT FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentlin Ver. 2.0
SEQ ID NO 1
LENGTH: 1337
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (170) .. (1066)
US-09-127-928-1

Query Match 93.3%; Score 1162.4; DB 3; Length 1337;
Best Local Similarity 95.7%; Pred. No. 2.2e-254; Indels 54; Gaps 1;
Matches 1227; Conservative 0; Mismatches 1;

QY 19 GGCAGGCTGTGCTATCTCTGCTGTCTCCAGAGTGGGCCCCGGAGGTCAAGAGCTCCAG 78
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QY 79 AAGGGCCAGCTGGGATATCTGAGATTGGCATTCAGCCCCCATTTTGTCTGCAAACTG 138
Db 89 AAGGGCCAGCTGGGATATCTGAGATTGGCATTCAGCCCCCATTTTGTCTGCAAACTG 148
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Db 149 GTCAAGGCAAGTGTCTCTCATGAGGAGCTTAAAGACAGTGGCAAGTGTCTGCAAGTGG 208
QY 199 CCACAGCCGAGCCACTGAGGAGCCGCTGATGCTTCAACGAGAGCCGCTGAGAGCCGAG 258
Db 209 CCACAGCCGAGCCACTGAGGAGCCGCTGATGCTTCAACGAGAGCCGCTGAGAGCCGAG 268
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QY 319 CAGATCTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 378
Db 329 CAGATCTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 388
QY 379 ACCTTGTCTGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 438
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QY 499 TTCCACACAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 558
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QY 559 TGGAGAGGCGGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 618
Db 569 TGGAGAGGCGGAGGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 628
QY 619 CTGCTCCGCTCAAAAGAGAGACTTGTCTCAAGTGTGAGAGAGACTCACTCCAGCTG 678
Db 629 CTGCTCCGCTCAAAAGAGAGACTTGTCTCAAGTGTGAGAGAGACTCACTCCAGCTG 688
QY 679 CTGAGGCTCTGAGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 738
Db 689 CTGAGGCTCTGAGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 748
QY 739 CTGAGGCTCTGAGAGCCCTGTCTCTAGGCTTGAGCACTTGAGAGCCCTGGAGCACTGATGGG 798
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QY 799 CAGAG----- 804
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Db 809 CAGAGCAGAGAGGGGTCAATCAAGCCAGAGGCCAGAGGGGCTGTGGTCTTGAAGCC 868
QY 805 CCAGAGCCAGAGGATGTGAGAGCCAGCTGGCGGCTGCAAGAGAGAGAGAGCTGCAAG 864
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Db 869 CCAGAGCCAGAGGATGTGAGAGCCAGCTGGCGGCTGCAAGAGAGAGAGAGCTGCAAG 928
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QY 865 GTGAGCTGAGACCGGCGGCTGATGCTTTGTGCGGCGGCTGCAAGAGAGAGAGAGCTG 924
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Db 929 GTGAGCTGAGACCGGCGGCTGATGCTTTGTGCGGCGGCTGCAAGAGAGAGAGAGCTG 988
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QY 925 GAGTGTGCCCCCGGCTGAGCTGTGCCCCATCTGAGAGAGAGAGAGAGAGAGAGAGCTG 984
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Db 989 GAGTGTGCCCCCGGCTGAGCTGTGCCCCATCTGAGAGAGAGAGAGAGAGAGAGAGCTG 1048
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QY 985 CGCACTTCTGTCCTTGAAGCCAGAGTGCATGAGCCGAGAGTGGAGTGGAGCTC 1044
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Db 1049 CGCACTTCTGTCCTTGAAGCCAGAGTGCATGAGCCGAGAGTGGAGTGGAGCTC 1108
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QY 1045 CTTGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1104
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QY 1105 TGTTCATTCAGACTGACAGCCCTGATTCGCCAGACAGCCAGAGGAGAGAGAGAG 1164
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Db 1169 TGTTCATTCAGACTGACAGCCCTGATTCGCCAGACAGCCAGAGGAGAGAGAGAG 1228
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QY 1165 CCCTTGTGCTGGCGTGGGAGATGCTTAAGTCTGTTGAGATGCTTGAATGAAAT 1224
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Db 1229 CCCTTGTGCTGGCGTGGGAGATGCTTAAGTCTGTTGAGATGCTTGAATGAAAT 1288
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QY 1225 AAGTGGTCTTTCCTTGAAGT 1246
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Db 1289 AAGTGGTCTTTCCTTGAAGT 1310
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RESULT 3
US-09-949-016-13691
; Sequence 13691, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13691
; LENGTH: 8572
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13691

Query Match 39.5%; Score 492.4; DB 3; Length 8572;
Best Local Similarity 99.8%; Pred. No. 3,4e-102;
Matches 493; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GGCAGGCTGTGCTTATCCTGCTGTCTCCAGAGGTGGGCGGCGGAGTCCAG 78
| | | | |
Db 203 GGCAGGCTGTGCTTATCCTGCTGTCTCCAGAGGTGGGCGGCGGAGTCCAG 2092
| | | | |
QY 79 AAGGCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCACTTCTGCTGCAAACTG 138
| | | | |

Db 2093 AAGGCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCACTTCTGCTGCAAACTG 2152
| | | | |
QY 139 GTCAGAGCCAGATGTCCTTCATAGGAGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAG 198
| | | | |
Db 2153 GTCAGAGCCAGATGTCCTTCATAGGAGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAG 2212
| | | | |
QY 199 CCAGAGCCAGAGCTGAG 258
| | | | |
Db 2213 CCAGAGCCAGAGCTGAG 2272
| | | | |
QY 259 TCTGTGGAG 318
| | | | |
Db 2273 TCTGTGGAG 2332
| | | | |
QY 319 CAGATCCTGGGAG 378
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Db 2333 CAGATCCTGGGAG 2392
| | | | |
QY 379 ACCTGTCCAG 438
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Db 2393 ACCTGTCCAG 2452
| | | | |
QY 439 TTTATGACTGAG 498
| | | | |
Db 2453 TTTATGACTGAG 2512
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QY 499 TTCCACAGAGGCCA 512
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Db 2513 TTCCACAGAGGCCA 2526
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RESULT 4
US-09-023-655-334
; Sequence 334, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Jeffrey J. Selthamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 334:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226 base pairs
; TYPE: nucleic acid

Db	450	AGCCCCAGGAGCCAGGAGATGTGAGAGCCAGCTGGCGGCTGTGAGGAGGAGAGAGCT	505
Qy	860	GCAAGGTGTGCTTCGAGACCGGCGGCTGTCCATGTCCTTTTGCCGTTGGCGGCACTGGTCT	915
Db	510	GCAAGGTGTGCTTCGAGACCGGCGGCTGTTCATGTCCTTTTGCCGTTGGCGGCACTGGTCT	565
Qy	920	GTCGTGAGTGGCCCCCGGCTTCAGACTGGC	951
Db	570	GTCGTGAGTGGCCCCCGGCTTCAGACTGTGC	601

RESULT 8
US-09-016-434-216
; Sequence 216, Application US/09016434
; Patent No. 6500938

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1      GENERAL INFORMATION:
2      APPLICANT: Janice Au-Young
3      APPLICANT: Jeffrey J. Sellmeier
4      TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
5      TITLE OF INVENTION: PATHWAY GENE EXPRESSION
6      NUMBER OF SEQUENCES: 1490
7      CORRESPONDENCE ADDRESS:
8      ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
9      STREET: 3174 PORTER DRIVE
10     CITY: PALO ALTO
11     STATE: CALIFORNIA
12     COUNTRY: USA
13     ZIP: 94304
14     COMPUTER READABLE FORM:
15     MEDIUM TYPE: Floppy disk
16     COMPUTER: IBM PC compatible
17     OPERATING SYSTEM: PC-DOS/MS-DOS
18     SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
19     CURRENT APPLICATION DATA:
20     APPLICATION NUMBER: US/09/016,434
21     FILING DATE: HERewith
22     CLASSIFICATION:
23     PRIOR APPLICATION DATA:
24     APPLICATION NUMBER:
25     FILING DATE:
26     CLASSIFICATION:
27     ATTORNEY/AGENT INFORMATION:
28     NAME: Zeller, Karen J
29     REGISTRATION NUMBER: 37,071
30     REFERENCE/DOCKET NUMBER: PA-0002 US
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: (650) 845-0555
33     TELEFAX: (650) 845-4166
34     INFORMATION FOR SEQ ID NO: 216:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 200 base pairs
37     TYPE: nucleic acid
38     STRANDEDNESS: single
39     TOPOLOGY: linear
40     IMMEDIATE SOURCE:
41     LIBRARY: BLADTUT04
42     CLONE: 1520835
43     US-09-016-434-216

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Query Match	10.8%	Score 135	DB 3	Length 200
Best Local Similarity	88.4%	Pred. No. 1.9e-21		
Matches 152	Conservative	0	Mismatches 19	Indels 1
QY	800	AGAGCCAGAGCCAGGATGTGAGCGCGACGCTGGCGCGCTGTCAGAGAGAGAGGAGCT	859	
Db	6	AGCCCCAGAGCCAGGAGATGTGAGCGCGCA-NTCGCGCGCTGCAGAGAGAGAGGAGCT	64	
QY	860	GCAAGGTGTGCTTGACCGCGCGCGTGCATGTCCTTTGTGCCGTGCGGCCACTTGTC	919	
Db	65	GCAAGTGTGCTTGAGACCGCGCGCGTGCATGTCCTTTGTGCCGTGCGGCCACTTGTC	124	
QY	920	GTGCTGATGTGCCCGCGCGCTGCACGCTGTGCCCATCTGCAGAGCCCCCGT	971	

Db
125 GTGCTGANTGTGCCCGGGCANNANCTTNCCTCCCAATTGNAAGCCCCCCT 176

RESULT 9
US-09-023-655-387
; Sequence 387, Application US/09023655

GENERAL INFORMATION:

APPLICANT: Susan G. Stuart

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:

STREET: 3174 PORTER DRIVE

STATE: CALIFORNIA

ZIP: 94304

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;
CURRENT APPLICATION DATA:

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FILED DATE: HEREWITH

PRIOR APPLICATION DATA:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 37,071

TELECOMMUNICATION INFORMATION:

TELEFAX: (650) 845-4166

SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs

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;
; type: nucleic acid
STRANDEDNESS: single

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IMMEDIATE SOURCE:

CLONE: 1520835

US-09-023-655-387

Query Match	Score	DB	Length
10.8%	135	3	200

Matches 152; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

800 AGGAGCCAGGAGCCAGGATGTGAGAGCCGACCTGCGGCGCTGCAGGAGGAGGACGT 859

Db 6 AGCCCCCAGGAGCCAGGGATGTGGAGGCGCA-NTGCCGCCGCTGCAGGAGGAGAGGACGT 64

860 GCAGGTGTGCTGGACCGCGGTGTCCATCGTCTTTGTGCGGTGCGGCACCTGGTCT 919

65 GCAGGGTGCCCGACCGCGGTCCTTGTCCGTCGCACCCTGGCT 124

[illegible]

Db 125 GTGCTGANTGTGCCCCCGGGC>NNNAANCTTNCCCCCATTTGNAAGGCCCCNT 176

RESULT 10

US-09-949-016-66134
; Sequence 66134, Application US/09949016


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Qy 522 GGTGAGGTGCTTCTTCTATGCGGCTTCAGAGCTGAGAGCGCGGAGACGCCCTG 581
Db 1163 TGTCAAGTGTCTTCTGCTGTGAGTGTGGCTGAGGTGCTGGAATCTGAGATGACCCCTG 1222
Qy 582 GACGAGCATGCCAAGTGTGTCCTCCAGCTGTCACTTCTGCTCCGTCGCAAAAGGAGAGA 641
Db 1223 GGTGAAACATGCCAAGTGTGTTCCAGGTGTGAGTACTTGTCTCAGAAATCAAAGGCCAAGA 1282
Qy 642 CTTTGTCCACAGTGTGAGAGACTCACTCCAGCTGCTG 682
Db 1283 ATTGTGAGCCAAAGTTCAGCTGGCTATCCTCATCTACTTG 1323

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Search completed: April 19, 2006, 23:46:01
 Job time : 262 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2006, 20:07:45 ; Search time 219 Seconds
(without alignments)
2508.066 Million cell updates/sec

Title: US-09-762-577B-12
Perfect score: 1721
Sequence: 1 MGPDSAKLHRGPQPSHMA.....GLOGLPAPLCLFWTFWMAC 309

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSMB.spool/US09762577/rnat_19042006_11133_24874/app_query.fasta.1
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-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
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3: /cgn2_6/pdata/1/ina/6 COMB.seq:*
4: /cgn2_6/pdata/1/ina/6A COMB.seq:*
5: /cgn2_6/pdata/1/ina/H COMB.seq:*
6: /cgn2_6/pdata/1/ina/PCPUS COMB.seq:*
7: /cgn2_6/pdata/1/ina/PP COMB.seq:*
8: /cgn2_6/pdata/1/ina/RE COMB.seq:*
9: /cgn2_6/pdata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1713	99.5	1260	3	US-09-949-016-1949	Sequence 1949, App
2	1694	98.4	1337	3	US-09-127-928-1	Sequence 1, Appl1
3	1030	59.8	8572	3	US-09-949-016-13691	Sequence 13691, A
4	478.5	27.8	2676	3	US-09-212-971-11	Sequence 11, Appl
5	478.5	27.8	2676	3	US-08-800-929A-11	Sequence 11, Appl
6	478.5	27.8	2676	3	US-09-617-053A-11	Sequence 11, Appl
7	472	27.4	2563	3	US-09-016-434-1076	Sequence 1076, App
8	472	27.4	2563	3	US-09-023-655-894	Sequence 894, App
9	472	27.4	2601	3	US-08-569-749-3	Sequence 3, Appl1

10	472	27.4	2601	3	US-09-689-366-3	Sequence 3, Appl1
11	472	27.4	2601	3	US-10-232-286-3	Sequence 3, Appl1
12	472	27.4	2601	6	PCT-US96-12860-3	Sequence 3, Appl1
13	472	27.4	3076	2	US-09-205-144-1	Sequence 1, Appl1
14	472	27.4	3076	3	US-09-814-915A-11	Sequence 11, Appl
15	472	27.4	3165	3	US-09-949-016-160	Sequence 160, App
16	472	27.4	3573	3	US-09-949-016-5007	Sequence 5007, App
17	472	27.4	6669	3	US-09-212-971-5	Sequence 5, Appl1
18	472	27.4	6669	3	US-08-800-929A-5	Sequence 5, Appl1
19	472	27.4	6669	3	US-09-617-053A-5	Sequence 5, Appl1
20	472	27.4	6669	3	US-09-617-17-230	Sequence 230, App
21	465	27.0	2676	2	US-08-511-485-5	Sequence 5, Appl1
22	465	27.0	2676	3	US-09-201-936-5	Sequence 5, Appl1
23	465	27.0	2676	3	US-09-011-356-5	Sequence 5, Appl1
24	465	27.0	2676	3	US-09-672-117-220	Sequence 220, App
25	465	27.0	2676	3	US-09-201-932-5	Sequence 5, Appl1
26	465	27.0	2862	3	US-08-569-749-13	Sequence 13, Appl
27	465	27.0	2862	3	US-09-689-366-13	Sequence 13, Appl
28	465	27.0	2862	3	US-10-232-286-13	Sequence 13, Appl
29	465	27.0	2862	6	PCT-US96-12860-13	Sequence 13, Appl
30	465	27.0	2916	3	US-09-814-915A-31	Sequence 31, Appl
31	463	26.9	3151	3	US-09-212-971-13	Sequence 13, Appl
32	463	26.9	3151	3	US-08-800-929A-13	Sequence 13, Appl
33	463	26.9	3151	3	US-09-617-053A-13	Sequence 13, Appl
34	462.5	26.9	1435	6	PCT-US95-05922A-1	Sequence 1, Appl1
35	462.5	26.9	2589	3	US-08-569-749-1	Sequence 1, Appl1
36	462.5	26.9	2589	3	US-09-689-366-1	Sequence 1, Appl1
37	462.5	26.9	2589	3	US-10-232-286-1	Sequence 1, Appl1
38	462.5	26.9	2589	6	PCT-US96-12860-1	Sequence 1, Appl1
39	462.5	26.9	3532	2	US-09-205-204-1	Sequence 1, Appl1
40	462.5	26.9	3732	3	US-09-212-971-7	Sequence 7, Appl1
41	462.5	26.9	3732	3	US-08-800-929A-7	Sequence 7, Appl1
42	462.5	26.9	3732	3	US-09-617-053A-7	Sequence 7, Appl1
43	461.5	26.8	2580	2	US-08-511-485-7	Sequence 7, Appl1
44	461.5	26.8	2580	3	US-09-201-936-7	Sequence 7, Appl1
45	461.5	26.8	2580	3	US-09-011-356-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-949-016-1949
; Sequence 1949, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1949
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1949

Alignment Scores:
Pred. No.: 4.34e-137
Score: 1713.00
Percent Similarity: 99.7%
Best Local Similarity: 99.7%
Query Match: 99.5%
DB: 3
Length: 1260
Matches: 1260
Conservative: 308
Mismatch: 0
Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) X US-09-949-016-1949 (1-1260)

Db	174	ATGGAGCCTAAAGACAGTCGCAAGTCTGCACCCGGAGCCACACCGCAAGCCTGGGCA	23
Qy	21	AlAGlYAspSglYprOthrGlnGluIuaArgCySGlYProIaYgSerLeuGlySerProValIleu	40
Db	234	GCCGGATGATGTCTCCACGGAGAGCGCTGTGAACCCCGCTCTGGGAGCGCTGTCTCTA	293
Qy	41	GlyLeuAspThrCySArGAlaTrpAspHisValaAspGlyGlnIleLeuGlyGlyLeuArg	60
Db	294	GGCTGTGACACCTGCAGAGCCTGGGACCAACGTGATGGGCAATCTTGAGCACTGGG	35
Qy	61	ProLeuThrGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgIYProAla	80
Db	354	CCCTTACAGAGAGAGAGAGAGAGAGAGGCGCGCGGGCACCTTGTCCAGGGGCGCTGCC	413
Qy	81	PheProGlyMeGlySerGluGluLeuArgLeuAlaSerPheIYAspTrpProLeuThr	100
Db	414	TTCGCCGGATGGGCTCTGAGAGATGGGTCTGGCGCTCTTCTATGACTGGCGCTGACT	473
Qy	101	AlaGluValProProGluIuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120
Db	474	GCTGAGTGCCACCCGAGCTGCTGCTGCTGCGGGCTTCTTCCACAGGCGATCAAGAC	533
Qy	121	LYsValArgCyPhePheCySerTrGlyXGlyLeuGlnSerTrpLYsArgGlyAspAspPro	140
Db	534	AAAGTGAGGTGCTTTCTTCTGCTATGGGGCGCTGCAGAGCTGGAAGCGCGGAGACCCC	593
Qy	141	TrpThrGluHisAlaLYsTrpPheProSerCyGlnPheLeuLeuArgSerLYsGlyArg	160
Db	594	TGGACGGAGCATGCGCAAGTGGTTCCCGACGTGATGCTTCTGCTCCGGCTCAAAAGAAAG	653
Qy	161	AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp	180
Db	654	GACTTGTTCACAGTGTCAAGAGACATCACTCCACGCTGCGGGCTCTTGGAGCCGTGG	713
Qy	181	GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTYrProGlu	200
Db	714	GAAAGAACGGAAAGACGACGCCCTGTGGCCCCCTCCCTCCCTGCTTGAGTACCTTGAG	773
Qy	201	LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGlyAlaArgAsp	220
Db	774	CTGCCACACCCAGAGAGAGAGTCAAGTCTGAAAGTCCACAGGACGACGAGGACCAAGAT	833
Qy	221	ValGluAlaGlnLeuArgArgLeuGlnGluGluThrCysAlaValCysLeuAspArg	240
Db	834	GTTGAGGGCGACGCTCGCGCGGCTCTCAAGAGAGAGAGACGTCGAAGGTGGCTGGACCGC	893
Qy	241	AlaValSerIleValPheValProCyGlyHisLeuValCysAlaGluCysAlaProGly	260
Db	894	GCCGTGTCCACGTCTTGTGTGCCTGGCGGCACCTGGTGTGTGCTAGAGTGGCCCCGGC	953
Qy	261	LeuGlnLeuCySProlIeCySArGAlaProValArgSerArgValaArgThrPheLeuSer	280
Db	954	CTGACAGCTGTGCCCATCTGCAAGAGCCCCCGTCCGACGCGCGGTGGCACTTTCCTGTCC	1013
Qy	281	***AlaArgCysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCyS	300
Db	1014	TAGCGCAGGTGCCATGTGCGCGGCGACGAGTGAGCTGCAAGTGGGTCCCTCCCTCTCTCC	1073
Qy	301	LeuPheTrpThrValaPheTrpAlaCyS	309
Db	1074	CTGTTCGAGACTGTGTCTGGGCTCG	1100

RESULT 2
US-09-12

Sequence 1, Application US/09127928
Patent No. 6472172
GENERAL INFORMATION:
APPLICANT: Deng, Gang
APPLICANT: Lin, Jiling-Huey

```

? APPLICANT: Morser, Michael J
? TITLE OF INVENTION: DNA Encoding a No. 6472172e1 Human Inhibitor-of-Apoptosis
? TITLE OF INVENTION: Protein
? FILE REFERENCE: DNA Encoding HIPA3
? CURRENT APPLICATION NUMBER: US/09/127,928
? CURRENT FILING DATE: 1998-07-31
? NUMBER OF SEQ ID NOS: 7
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO: 1
? LENGTH: 1937
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (170)..(1066)
US-09-127-928-1

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Alignment Scores:

Pred. No.:	1,976-135	Length:	133
Score:	1694.00	Matches:	308
Percent Similarity:	94.2%	Conservative:	0
Best Local Similarity:	94.2%	Mismatches:	1
Query Match:	98.4%	Indels:	18
DB:	3	Gaps:	1

US-09-762-577B-12 (1-309) X US-09-127-928-1 (1-1337

QY	1	MetGlyProLysAspSerLAlaValCysLeuHISaGVGILYProGlnProSerHIStrpAla	20
Db	170	ATGGAGACCTAAAGACAGTGTCCAAAGTGTCTGCACCTGTGAACCAACACCGACCACTGGGCA	22
QY	21	AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu	40
Db	230	GCCGGTGAATGTGCCACGACGAGGCGCTGTGGACCCCGCTCTGTGGACGCGTGTCTTA	28
QY	41	GlyLeuAspThrCysArgAlaTrpAspHisValaAspGlyGlnIleLeuGlyGlnLeuArg	60
Db	290	GGCTGTGACACTGGACAGACCTGGAGCCACGTGGATGGAGATCTGGGGCACTGGG	34
QY	61	ProLeuThrGlnGluGluGluGluGluValaGlyAlaThrLeuSerArgGlyProAla	80
Db	350	CCCTGCACAGAGAGAGAGAGAGAGAGGCGCCGGGGGCACCTTGTCCAGGGGGCTGCC	40
QY	81	PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyraAspTrpProLeuThr	100
Db	410	TTCCCGGCAATGGGTCTGAAGAAATGGTGTGGCTCTTCCTCTTAATGACTGGCCCTGACT	46
QY	101	AlaGluValaProProGluLeuLeuAlaAlaGlyPhePheHIStrpGlnHisGlnAsp	120
Db	470	GCTGAGGTGCCACCGAGCTGTCTGGCTGTCCGGCTTCTTCACACAGGCGACACAGAC	52
QY	121	LysValaArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgIlyAspAspPro	140
Db	530	AAGGTGAGGTCTTCTTCTGTCTTAATGGGGGCTGCAGACGTGAAGCGCGGGAGACCCC	58
QY	141	TrpThrGlnHisAlaIlystrPhePheProSerCysGlnPheLeuLeuAspSerLysGlyArg	160
Db	550	TGAGCGAGCAATGCCAAGTGTCTCCAGCTGTCAATCTGTCTCCGCTCAAAAGGAAGA	64
QY	161	AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp	180
Db	650	GACTTTGTCCACAGTGTGCGAGAACTCACTCCACAGCTGTGGGCTTTGGGACCGGTGG	70
QY	181	GluGluProGluuAspAlaAlaProValAlaProSerValProAlaSerGlyTyProGlu	200
Db	710	GAAGAAACCGGAAGACGAGCCCTGTGTGCCCTCCCTCCCTGCTGTGGGTACCCAGAG	76
QY	201	LeuProThrProArgArgGlyValaGlnSerGlnSerLysGlnGlu	220
Db	770	CTGCCACACACCCAGAGAGAGGTCTCAATCTGAAGATGCCAGAGGCCAGAGGGGTCACT	82
QY	216	-----ProGlyAlaArgAspValaGlu	222

Db 830 CCACCGAGGCCAGAGGGCCTGTGGCTTTAGCCCCCAGAGACCAGGATGTGAG 889
 Qy 223 AAGlnleuAArgATgLeuGlnGluArgThrcyslysvAlCysleuAspArgAlaVal 242
 Db 890 GCGAGCTGGCGCGCTGACAGAGAGAGAGCTGCAAGGTGTGCTGTGACCGCGCTG 949
 Qy 243 SerlleValPheValProCysGlyHisleuValCysAlaGluCysAlaProGlyLeuGln 262
 Db 950 TCCATCGCTTTGTCGCGTGGCGCCACTGTGTGTGTGATGTGTGCCCCGGCCTGACG 1009
 Qy 263 LeuCySProlleCysArgAlaProValArgSerArgValArgThrPheLeuSer***Ala 282
 Db 1010 CTGAGCCCATCTGACAGAGCCCGCTCCGACCGCGCTGCGCACCTTCTGCTTAAGCC 1069
 Qy 283 ArgCysHisGlyAArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCysleuPhe 302
 Db 1070 AGGTGCCATGGCCCGGACAGGTGGCTGCAAGTGGCTCTGCGCCCTCTGTGCTGTTC 1129
 Qy 303 TrpThrValPheTrpAlaCys 309
 Db 1130 TGAAGTGTCTGGGCTGC 1150

RESULT 3

US-09-949-016-13691
 ; Sequence 13691, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 13691
 ; LENGTH: 8572
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-13691

Alignment Scores:

Pred. No.: 1.27e-77 Length: 8572
 Score: 1030.00 Matches: 306
 Percent Similarity: 21.7% Conservative: 1
 Best Local Similarity: 21.6% Mismatches: 2
 Query Match: 59.8% Indels: 1107
 Gaps: 6

US-09-762-577b-12 (1-309) x US-09-949-016-13691 (1-8572)

Qy 1 MetGlyProlyAspSerAlaValCysleuHisArgGlyProGlnProSerHisTrpAla 20
 Db 2174 ATGGAGCTTAAGACAGATGCTCAAGTGTCTGACCGTGGACACAGCCGACCACTGGGCA 2233
 Qy 21 AAGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 Db 2234 GCGGCTGATGTGCTCCAGCAGAGAGCGCTGTGAGACCCGCTCTCTGGGACGCTGTCTA 2293
 Qy 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 Db 2294 GGGCTGGACACCTGACAGAGCTGGGACCACTGGATGGCAGATCTGGGCGCAGCTGGCG 2353
 Qy 61 ProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGln 80
 Db 2354 CCCCTGACAG 2413

Qy - 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
 Db 2414 TTCCCGGAGATGGGCTGTGAGAGATGGCTGTGGCTCTTCTATGATGAGCCGCTACT 2473
 Qy 101 AAGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThr 116
 Db 2474 GCTGAGGTGCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2532
 Qy 116 ----- 116
 Db 2533 GCGGGGGGGGCTTCTGCTGCGTGGGCTGTGGGACAGATTGTGACCTTTCAGCCAGGGC 2592
 Qy 116 ----- 116
 Db 2593 TGTGCTCTCTCGTAGCATCCATCCCCCAAGAGAGGTCTGCGCTGATGAGAGAGAG 2652
 Qy 116 ----- 116
 Db 2653 TGGTCTGCAAGCCCTCCAGTCCCATGGGCTGTGCTGTGACACCTCTCCCGAGTCT 2712
 Qy 116 ----- 116
 Db 2713 CTGCTGCTGAGTGTTCAGACCGTGGAGCTGAGAGAGGGGCTGCTTGGACACAGTCT 2772
 Qy 116 ----- 116
 Db 2773 GAGGCTCAGCTGTGAGAGCGCCAGCTTGTGTGACAGTACCCCTTTGTGATAGAGT 2832
 Qy 116 ----- 116
 Db 2833 GGGTGGGGCTGACATTCCTGCGGGCCCTCATTCCCGCTGCTGTTCGACAGAGAGA 2892
 Qy 116 ----- 116
 Db 2893 GGAGATGTTTAAAGAACAGAGATCAGGATGACCAAGGAGGAGTGTGACCCAGAGGTC 2952
 Qy 116 ----- 116
 Db 2953 CTGATGCTCAGCTGTGGGAAATTTCTCAGAGCCCACTGACAGTACTGTGTCT 3012
 Qy 116 ----- 116
 Db 3013 TCCCAACTGATCAATCAATCCCGAGAGTACCTATCTAGTCTTGGCCCGGCTGTCTTC 3072
 Qy 116 ----- 116
 Db 3073 TGCCTTACAGCTGACAGACCATGTGTGACAGCTGAGTTCAGGCTTGCACCTTC 3132
 Qy 116 ----- 116
 Db 3133 CTGGCTGAAGAGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3192
 Qy 116 ----- 116
 Db 3193 GGTCAATTCAGAGAGTGGGCTGTGGGGGAGACCATCTGTGTAAGGCTGGACCACTTAA 3252
 Qy 116 ----- 116
 Db 3253 GACAGCTGTGCGGGGAGACAGTGTGGGACAGTCAAGACCGTGGCTGTAAGGGGAGG 3312
 Qy 116 ----- 116
 Db 3313 CCCAGTCAACCACTTCCTGGAAGTCAAGGCTCAGAGAGCAAGAGCCAGGAGAGG 3372
 Qy 116 ----- 116
 Db 3373 ATGGCAGGTGAGAGAGCGGGGCTTTTGGGGCTGTGAGAGTCCAGTCCGATGAGAGCC 3432
 Qy 116 ----- 116
 Db 3433 AAACCTGTATGATGAGTGCAGGTGACGTATGATGATGATGATGATGATGATGATGATG 3492
 Qy 116 ----- 116

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Db 3493 GCCAGAGGTAGAGATGACGGGTCCGCCACCCCAAGGAGCATGAGTTCTTAAA 3552
QY 116 -----
Db 3553 GCAAGCTGGCCCCAGACTGGCTTCTAGGCGAGCTCCTTCTTCTCACTGGAAAT 3612
QY 116 -----
Db 3613 CCATCTGGGGAAGAGAGACCTGGGAGGGGCCCTTGGCTCTGAGGCCCAAGGCT 3672
QY 116 -----
Db 3673 ATAGATGACCAAGCCCTGGGGGCCCCCACTGCTCACTCTGGGAACAATGCAATGCA 3732
QY 116 -----
Db 3733 GCTCAGTCTTCTTGAACATTCTGGCCATCTGGCCGAGCACCCACTGTC 3792
QY 116 -----
Db 3793 CTTTTCACCTTGTATGCTAATGAGGTACAGTGAATCCCCCAACAAGCCCTGGCCA 3852
QY 116 -----
Db 3853 CCCCCTCTCTTCTTGGCACTGGAGCTCCCTCCAGCTGAAGCTCTCATAGCCTTGG 3912
QY 116 -----
Db 3913 AAGCACACCGGGGGCCCCGGGACCTGGGTGGACCTGGCTGGGGCCAGCATCTCTCCG 3972
QY 117 -----
Db 3973 ACCCCAGGCTATCGAGCAAGGTGAGTGTCTTCTGCTATGGGGCTGGCAGAGCTGG 4032
QY 135 LysArgGlyAspAspProTyrThrGluHisAlaValSerPhePro----- 149
Db 4033 AAGCGGGGGAGCGACCCCTGGACGGAGCATGCCAAGTGTCCCAAGTACCGGCTGGCC 4092
QY 149 -----
Db 4093 CTGGGGGCCCCGGGTCTGATCATGGGTAGGGGTGGCCCCCAAGGCTCTGTCAACC 4152
QY 149 -----
Db 4153 AACACAGGCTGCTTGTCTCTCTGGCCCCACAGGGCACTGGGAGGCCCTTCTGGGG 4212
QY 149 -----
Db 4213 AGGTGCTTCTGGCCGAGGTACCACTTTCTGTGAGGGCCCTTTTGGAAAGGCTG 4272
QY 149 -----
Db 4273 CTGGGGGAGAAATGCTCTCTCCATGGGACTACCTGAAGCCCATGAGAGGCTCTCAC 4332
QY 149 -----
Db 4333 AGCAGCCCTCTGGCCCATGCCCCAGGGCACTGCAAGGTGGCGGAGAGGGGGCCCAAC 4392
QY 149 -----
Db 4393 CCTGACCCCCGGGATCCAAAGGCTTGAAGCAGACAGTGGGGGCCCTGAACCCCAACTA 4452
QY 150 -----
Db 4453 CATCTCTGGGGCATCTGCAAGCTGTCAAGTCTGCTCCGGTCAAAAGAGAGACTTGTG 4512
QY 164 HisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyr----- 177
Db 4513 CACAGTGTCAAGAGACTCACTCCCAAGCTGCTGGGCTCTTGGGTACGCGCCACTCTCT 4572
QY 177 -----
Db 177 -----

Db 4573 CGGGCTCCGGGTGGCAGTGGGGTCTGCCCTCTTATTTCCCAAGGCTGATGCTTC 4632
QY 178 -----
Db 4633 TGGCTCTTCAAGGACCCGTGGGAAGACCGAAGACGACGCCCTGTGGCCCCCTCCGG 4692
QY 192 -----
Db 4693 TGAGAGTGAACAACACCCTGTGACTCTTGTGGGCTGTCAGAGCTGTCTTGGCCAAAG 4752
QY 192 -----
Db 4753 CCAGTGGTGTCCCAACCTCCCAAGACAGAGAGAGTGAACGGCATGTGACAGGTGT 4812
QY 192 -----
Db 4813 GACGCTGCTGGGTGGCTTCAAGGGGCTGTGCCATGTGAGGGTGGGGCGGGGCGG 4872
QY 192 -----
Db 4873 CAGGGGCTCCCCAGTGCAGAGCCCATTTCTGCTTCTCCAGCTTACCCCTTGGCA 4932
QY 192 -----
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QY 192 -----
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QY 192 -----
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QY 192 -----
Db 5113 CGGGGATCTGTGAGACCCCTCCACTCCCGGCAGAACTGGACCCCAAGCTGCAAGCC 5172
QY 192 -----
Db 5173 TGTATCTGGGCGGGGCCACTTTCTCTTGGAGTTAGGCTCAAGTCTATCTTAACTGT 5232
QY 193 -----
Db 5233 CCAAGTCTCCGCTCTGGGTGACCTTGAAGCTGACCTGACCAACCAAGAGAGAGTCAAGTCTG 5292
QY 211 LysSerAlaGlnGlu----- 215
Db 5293 AAAAGTCCAGAGACCAAGTGCAGAGCCGGGACCCCTGGGTGAGGCTGGGCAAGGGA 5352
QY 215 -----
Db 5353 GGGGTAGGAGACCCCGACCTTCCATGAGCCCATAGAGGTGGGGCCAGAGGTGTGGGACA 5412
QY 215 -----
Db 5413 TTTGCAGGCTGTCTCTTAGAGAGGGGTCAAGTCAAGCCGAGGCCAAGAGGGGTGTGG 5472
QY 216 -----
Db 5473 GTTCTTAGCCCCCAGAGGCAAGGATGTGAGGCCCAAGTGTGGGGCGGCTGCAAGGGAG 5532
QY 232 ArgThrCysIleValCysLeuAspArgAlaValSerIleValPheValProCysGlyHis 251
Db 5533 AGGACGTGCAAGGTGTGGCTGGACCCGCGGTGTCCATGCTCTTTTGTGCGGTGGCCAC 5592
QY 252 LeuValCysAlaGluCysAlaProGlyLeuGlnLeuCysProIleCysAlaArgAlaProVal 271
Db 5593 CTGGTCTGTGCTAAGTGTGTGCCCCCGGCTGCAAGCTGTGCCCCATGCAAGAGCCCCGTC 5652
QY 272 ArgSerArgValArgThrPheLeu----- 279
Db 5653 CGCAGCCGCTGGCCACTTTCCTGTCTTAGGCCAAGTGAAGCCCCCAAGACCAAGCGGAG 5712
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Qy 279 ----- 279
Db 5713 CCAGCCCTCTGCGAGGGGGCCCTGAGCCGCTGTGCCGGCCCTCTGTAACCATGCA 5772
Qy 279 ----- 279
Db 5773 GGGCCCTTCCGGGTGGAGCGCTGAGCTTTTATTAACCGGCTCCAGGTCCCGTGAATAG 5832
Qy 279 ----- 279
Db 5833 CGCCCATCATTTACTACTACCTCCCTTGACGCTTAGGTTGGGGCCCTGGTCTTGCGGCAAC 5892
Qy 279 ----- 279
Db 5893 GTGCCCTGCGCGCACCATAGCTGTGCTGCTGATTAAGTGAAGCGCTGTGGCTCTC 5952
Qy 279 ----- 279
Db 5953 TCAGCCTTGATTTTCTCAAGTGTCAAGAAAGCCGCTTTGAGCGCTTTGGGAAACA 6012
Qy 279 ----- 279
Db 6013 GGGTGGCCAGGTTGGGCTTACACAGCGAGACACTGGCCTTGCTTCAACCCGGGGCCAA 6072
Qy 279 ----- 279
Db 6073 GGCATGTGGGACACCTGACCGGGAAGGGGTGTGGAACCTGTCTTAGAGAAGTGG 6132
Qy 279 ----- 279
Db 6133 TGGATACCCCATCTGACGCGAGGAGACAGTGTGTGACGCGCTCGGGGCTCCCAAGAC 6192
Qy 279 ----- 279
Db 6193 CTCTGTAGTTACCCCGGAGTGTCTGAAGATCTGGCAGGGGCAAAAGTGTGGGACG 6252
Qy 279 ----- 279
Db 6253 GGAACCTGGGATCTGAGGCCCCCTGGCTAGGTGGCCCCCGTGGTTCATTAAGTCAAC 6312
Qy 280 -----Ser***AlaArgCysHisGlyArgProGlyLeuGlnSerGlyLeuPro 286
Db 6313 CACCCCTCTCTCCCTCTAGGTGTGCATGGCCGCGCAGTGGGCTGCGAGAGTGGGCTCCCT 6372
Qy 297 AlaProLeuCysLeuPheThrValPheThrAlaCys 309
Db 6373 GCCCTCTGTGCTGTCTGTGACTGTGTCTGGGCTGC 6411

RESULT 4
US-09-212-971-11
; Sequence 11, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneiluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Teang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; EARLIER FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-212-971-11

Alignment Scores:
Pred. No.: 3 33e-31 Length: 2676
Score: 478.50 Matches: 132
Percent Similarity: 37.5% Conservative: 40
Best Local Similarity: 28.8% Mismatches: 96
Query Match: 27.8% Indels: 192
DB: 3 Gaps: 11

US-09-762-577b-12 (1-309) x US-09-212-971-11 (1-2676)

Qy 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 885 ATAGGACCTGAGATAGAGTGGCTGTGGCGATGGGAAACTGAGCAACTGAGCAACTGGGA 944
Qy 21 AlaGlyAspGlyProThrGlnGlu-----ArgCysGlyProArgSerLeuGlySerPro 38
Db 945 CGTAGAGATGATCTATGTCAGAGACACAGAGGCAATTTCCCTC----- 986
Qy 39 ValLeuGlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGln 58
Db 987 -----ACGTCT----- 992
Qy 59 LeuArgProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 78
Db 993 -----CGTTTAAAGACTTGGGCTGAGTGTGCTTGCAGATACACTGTCTTAAC----- 1043
Qy 79 ProAlaPheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 98
Db 1044 -----CTGACATGACACACACGACCCCGATTAAGACATTTCTTAACCTGGCT 1094
Qy 99 LeuThrAlaGluValAlaProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlnHis 118
Db 1095 TCTAGTGCACACTGATTCATTCCTCCAGAACTTGCAAGTGGGCTTTTATTATACAGGACAC 1154
Qy 119 GlnAspLysValArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgGlyAsp 138
Db 1155 AGGATGATGTCAAGTGTCTTCTGTGATGCGTGGCTGAGTGTGGGAAATCGGAGAT 1214
Qy 139 AspProTrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuAspGlySer 158
Db 1215 GACCCCTGGGTGGAACATGCCAAGTGTTCCAAGGTGTGATGATCTTGCACAAATCAAA 1274
Qy 159 GlyArgAspPheValHisSerValGlnGlnIleThrHis-----SerGlnLeuLeu 174
Db 1275 GGCAGAAATTTTGTTCAGCCCAAGTTCAGCTGGCTATTCCTCATTTACTTGAAGCTATTTA 1334
Qy 175 GlySerTrpAsp---ProTrpGlnGlnProGlnAspAlaAlaProVal----- 189
Db 1335 TCTAGCTCAGACTCCCCAGAAATGAGATGAGAGAGCAATCGATTTTGGCCCT 1394
Qy 190 -----AlaProSerValProAlaSer----- 196
Db 1395 GAGAAAGTTCCGAAAGATGTGTCATGATGAGACACCGCTGTGTTAAACGACCTTGAA 1454
Qy 196 ----- 196
Db 1455 ATGGGCTTCAGTAGAGCGCTGGTGAACAGACGCTTCAAGCGGATTCCTGGCCACTGGT 1514
Qy 197 -----GlyTyrrProGluLeuProThrProArg 205
Db 1515 GAGAACTACAGACCGCTCAGTACCTGTTATAGCTTACTGATCAGAAAGACGAGATG 1574
Qy 206 ArgGlnValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp----- 220
Db 1575 AGAGAGAGCAGATGAGAGAGCGGCCGAGAGAGAGAGTATGATATGATGATATGATATC 1634

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QY 220 ----- 220
Db 1635 CGAAGAACAAATGTTGTTTCCAGATTGAGTGTGACCAATGCTGATTC 1634
QY 220 ----- 220
Db 1695 CTCCTAAGTCAAGGCGCATCATCTGACAGAGTGCATGCTGTGAAACAGAAACACAC 1754
QY 220 ----- 220
Db 1755 ACCTTACAGACAGACACTGATTTGATCTGTGTTAGCAAAAAGAACACTGCAGCAACC 1814
QY 220 ----- 220
Db 1815 TCATTAGAAATCCCTTCGGGAAATTGACCTGGGTTATACAGATATATTGTGCCA 1874
QY 221 -----ValGluAlaGlnLeu 225
Db 1875 CAGGACATTAGAGCTTCCACAGANGACATTGCGCTTACCAATGGAAGAACAGTTG 1934
QY 226 ArgArgLeuGlnGluArgThrCysLeuValCysLeuAspArgAlaValSerLeuAl 245
Db 1935 CGGAACCTCCAGAGGAAAGATGTAAAGTGTATGACCGAAGAGTATCCATCGTG 1994
QY 246 PheValProCysGlyHisLeu---ValCysAlaGluCysAlaProGlyLeuGlnLeuCys 264
Db 1995 TTCATTCCTGTGGCCATCTGGTGTGTGCAAAAGACTGCGCTCTCTGAGGAAGTGT 2054
QY 265 ProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer***AlaArg--- 283
Db 2055 CCCATCTGTAGAGGACCATCAAGGACAGGACAGTGGCATTTCTCTCTGAACAGACTA 2114
QY 284 -----CysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaPro 298
Db 2115 ATGGTTCATGAGCTGCAACTT-CAGCCAGAGGAAGTTCACTGTCATCCAGCTCCA 2170

RESULT 5
US-08-800-929A-11
Sequence 11: Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratic, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:

```

```

NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-800-929A-11

Alignment Scores:
Pred. No.: 3,336-31 Length: 2676
Score: 478.50 Matches: 132
Percent Similarity: 37.5% Conservative: 40
Best Local Similarity: 28.8% Mismatches: 96
Query Match: 27.8% Indels: 192
DB: 3 Gaps: 11

US-09-762-577B-12 (1-309) x US-08-800-929A-11 (1-2676)
QY 1 MetGlyProIlyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 885 ATAGGACCTGGAGATAGAGTGGCCCTTTCGTCGATGGGAAACTGCAACTGGGAA 944
QY 21 AlaGlyAspGlyProThrGlnGlu-----ArgCysGlyProArgSerLeuGlySerPro 38
Db 945 CGTAGAGATGATGCTATGTCAGAGCAGCAGGAGCATTTCCCTC----- 986
QY 39 ValLeuGlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGln 58
Db 987 -----AGCTGT----- 992
QY 59 LeuArgProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 78
Db 993 -----CCGTTCTTAAAGACTTGGGTGACGTGCTCGAGATACACTGCTCTTAC- 1043
QY 79 ProAlaPheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTrpAspTrpPro 98
Db 1044 -----CTGACATGACAGACACAGCAGCCCGTATTGAACTTCTTAACTGACCT 1094
QY 99 LeuThrAlaGluValProProGlnLeuAlaAlaAlaGlyPhePheHisThrGlyHis 118
Db 1095 TCTAGTGCATAGTTCAATTCACAGAACTTGCAAGTGGCGGCTTTTATATACAGACAC 1154
QY 119 GluAspLysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAsp 138
Db 1155 AGTATATATGCAAGATGTTTTTGTGCTGATGATGTGGCTGAGGTGGGAATGTGAGAT 1214
QY 139 AspProTrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuAspArgSerLys 158
Db 1215 GACCCCTGGGTGGAACATGCAAGTGTTCCTCAAGGTGATGACTTCTCAATAACAA 1274
QY 159 GlyArgAspPheValHisSerValGlnGlnThrHis-----SerGlnLeuLeu 174
Db 1275 GGCAGAAATTTGTGACCAAGATTCAGCTGAGCTGATCTCATCTTGAAGCAGATTA 1334
QY 175 GlySerTrpAsp---ProTrpGlnGlnProGlnAspAlaAlaProVal----- 189
Db 1335 TCTACGTCAACATCCCGCAAGAAATGAAATGACAGACCAATCGTTCATTGGCCCT 1394
QY 190 -----AlaProSerValProAlaSer----- 196
Db 1395 GGAGAAAGTTGGAGAGATGTCATGATGAGCAGCCGTGTGTTAAACAGACGCTTGAA 1454
QY 196 ----- 196
Db 1455 ATGGGCTTCAGTAGGAGCTGTTGAGAGACAGCGTTCAAGCGGCAAGTCTTGCCACTGTGT 1514

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QY 220 ----- 220
Db 1755 ACCTTACAAGACGACACTGATGTGTACTGTGTAAGAAAAGAAACACTGCAGCAACC 1814
QY 220 ----- 220
Db 1815 TCATTCAAGAACTCCCTTCGGAAATGACCCCTGCTTATACAGATATATTGTGCAA 1874
QY 221 ----- ValGluAlaGluLeu 225
Db 1875 CAGACATTAGGAGTCTTCCACAGATGACATTCGAGCTTACCAATGTAAGAAACAGTTG 1934
QY 226 ArgAglLeuGlnGluGlnAArgThrCysLeuAspArgAlaValSerIleVal 245
Db 1935 CGGAAGCTCCAGAGAGAAAGATGTGTAAGTGTATGACCCAGAGAGTATTCATGCTG 1994
QY 246 PheValProCysGlyHisLeu---ValCysAlaGluCysAlaProGlyLeuGlnLeuCys 264
Db 1995 TTCATTCCTGTGGCCATCTGTGTGTGTGCAAGACTGCGCTCTCTCTGAGAGAGTGT 2054
QY 265 ProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer***AlaArg--- 283
Db 2055 CCCATCTGTAGAGGACCATCAGGACAGGACAGTGGCAGCATTTCTCTCTGAAACAGACTA 2114
QY 284 ----- CysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaPro 298
Db 2115 ATGGTCATGCTGCAACTT-CAGCCAGAGAAAGTTCACTGTCACTCCAGCTCCA 2170

RESULT 7
US-09-016-434-1076
; Sequence 1076, Application US/09016434
; Patent No. 650938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1076:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2563 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

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; CLONE: g1160974
US-09-016-434-1076
Alignment Scores:
Pred. No.: 1,13e-30
Score: 472.00
Percent Similarity: 37.7%
Best Local Similarity: 26.9%
Query Match: 27.4%
DB: 3
Gaps: 11

US-09-762-577B-12 (1-309) x US-09-016-434-1076 (1-2563)
QY 1 MetGlyProLeuAspSerAlaValCysLeuHisArgGlyProGlnProSerHisTyrAla 20
Db 711 ATAGGACCTCGAGAGACAGAGTGGCTTGTGCTGTGGTGGAAATGAGCAATTGGGAA 770
QY 21 AlaGlyAspGlyProThrGlnGlu-----ArgCysGlyProArgSerLeuGlySerPro 38
Db 771 CCGAAGATTAATGCTATGTCAGAACACCTGAGACATTTCCCAA----- 815
QY 39 ValLeuGlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGln 58
Db 816 -----TGC----- 818
QY 59 LeuArgProLeuThrGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 78
Db 819 -----CCATTATAGAAATCAAGCTTCAAGACCTTCAAGATACACAGTTCTTAAT--- 869
QY 79 ProAlaPheProGlyMetGlySerGlyLeuLeuArgLeuAlaSerPheTyrAspTyrPro 98
Db 870 -----CTGAGATGCAAGACACATGACACCCGCTTAACATTTTAACTGGGCC 920
QY 99 LeuThrAlaGluValProProGlyLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHis 118
Db 921 TCTAGTGTTCAGTTAATCTGAGCAGCTTCAAGTGGGCTTTTATATATGGGTAAAC 980
QY 119 GlnAspLeuValArgCysPhePheCysPheGlyGlyLeuGlnSerTyrPheArgGlyAsp 138
Db 981 AGTATGATGTCMAATGCTTTTGGCTGTGATGTGACCTCAGCTTGGGAATCTGAGAT 1040
QY 139 AspProTyrPheGlnHisAlaValTyrPheProSerCysGlnPheLeuLeuArgSerIle 158
Db 1041 GATCCATGGGTTCACAAATGCCAAGTGTTCAGAGTGTGAGTCTTGATTAAGATTAA 1100
QY 159 GlyArgAspPheValHisSerValGlnGluThrHisSerGlnLeuGlySer----- 176
Db 1101 GAGCAGAGTTCATCCGTCAAGTTCAGAGCTTCACTCATCTTAAGAACAGCTGCTA 1160
QY 177 -----TTPAspPro 179
Db 1161 TCCACATCAGACAGCCAGAGATGAAATGACAGATCAATTAATCCATTTTGAACCT 1220
QY 180 TyrGluGlu---ProGluAspAla-----AlaProValAlaProSerValPro 194
Db 1221 GGAAGAGACCATTCAGAAAGATGCAATCATGATGAATATCTCTGATTAATGCGCGG 1280
QY 195 AlaSerGlyTyrProGlu-----LeuProThr 203
Db 1281 GAATGGGCTTATAGTAGAAGCTGTGTAACACAGAGTTTCAGAGAAAATCTTAGCAACT 1340
QY 204 Pro----- 204
Db 1341 GAGAGAAATTATAGACTAGTCATGATCTTGTGTAGACTTACTCAATGACAGAGATGAA 1400
QY 205 ---ArgArgGluValGlnSerGluSerAlaGlnGluProGlyValAlaArgAsp----- 220
Db 1401 ATAAAGGAGAGAGAGAGAAAGACAACTAGAGAAAAAGAAATCAATATGTTTATATTA 1460
QY 220 ----- 220
Db 1461 ATCCGAGAAATGAATGGACATTTTCAACATTTGACTTGTGTAAATTCCAATCTCGAT 1520

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QY 220 ----- 220
 Db 1521 AGCTACTACTGCCGGAATTATTATGAAACAAGACATGATTATTAAACAGAGACA 1580
 QY 220 ----- 220
 Db 1581 CAGAGCTCTTAAACAAGAAAGAACTGATTGATACGATTTTAAAGAAATATGCA 1640
 QY 220 ----- 220
 Db 1641 GCCACTGATTCAGAAACTCTGCAAGAGCTGAGCTGTTATATGACATTATTT 1700
 QY 221 ----- ValGluAa 223
 Db 1701 GTGCACACGACATTAATATATTCACAGAGATGTTTCAGATCTACAGTGGAGAA 1760
 QY 224 GlnleuAArgleuGlnGlnGluArgThrCysleuSerValCysleuSerAlaValSer 243
 Db 1761 CAATTGCGGACACTACAAAGAAAGAAACATGTAAGTGTATGCAAGAAAGTGTCC 1820
 QY 244 IleValPheValProCysGlyHisleu---ValCysAlaGluCysAlaProGlyLeuGln 262
 Db 1821 ATAGTGTATTCTCTTGCGTCACTAGTATGCAAGATGTGCTCTCTTTTAAAGA 1880
 QY 263 LeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 Db 1881 AAGTGCTCTATTGTAGAGATCAATCAAGGTAAGTGTGATCTTTCTTTCA 1934
 RESULT 8
 US-09-023-655-894
 ; Sequence 894, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023.655
 ; FILING DATE: HERewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 894:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2563 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:

; LIBRARY: GENBANK
 ; CLONE: G1160974
 ; US-09-023-655-894
 Alignment Scores:
 Pred. No.: 1,13e-30 Length: 2563
 Score: 472.00 Matches: 118
 Percent Similarity: 37.7% Conservative: 47
 Best Local Similarity: 26.9% Mismatches: 85
 Query Match: 27.4% Indels: 188
 Gaps: 11
 US-09-762-577b-12 (1-309) x US-09-023-655-894 (1-2563)
 QY 1 MetGlyProIleuSerSerAlaValCysleuHisArgIleProGlnProSerHisTrpAla 20
 Db 711 ATAGACCTGAGACAGAGTGGCTTGGCTTGGCTGAGAAATGAGCAATTTGGAA 770
 QY 21 AlaGlyAspGlyProThrGlnGlu---ArgCysGlyProArgSerLeuGlySerPro 38
 Db 771 CCGAAGATATATGCTATGTCAGAAACACCTGACATTTCCCAA----- 815
 QY 39 ValLeuGlyLeuSerThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGln 58
 Db 816 -----TTC----- 818
 QY 59 LeuArgProIleuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 78
 Db 819 -----CCATTATTAAGAAATCAAGCTTCAAGACACTTCAAGATACACAGTTTCTAAT--- 869
 QY 79 ProAlaPheProGlyMetGlySerGlnLeuArgLeuAlaSerPheTyrrAspTrpPro 98
 Db 870 -----CTGACGATGACAGACACATGACGCCCGCTTTAAACATTTTAACTGCGCC 920
 QY 99 LeuThrAlaGluValProProGlnLeuLeuAlaAlaIleArgPhePheHisTrpGlyHis 118
 Db 921 TCTAGTGTCTAGTATCTCTGAGCAGCTTCAAGACGGGTTTATATATGCGGTAAAC 980
 QY 119 GlnAspIleValArgCysPhePheCysGlyGlyGlyGlnGlnGlnGlnGlnGlnGlnGln 138
 Db 981 AGTGAATGATGTCAAAGCTTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1040
 QY 139 AspProThrThrGlnHisAlaIleTrpPheProSerCysGlnPheLeuLeuArgSerIle 158
 Db 1041 GATCCATGCGTTCACATGCGCAAGTGGTTTCCAAAGTGTAGTACTTGATTAAGATTTAA 1100
 QY 159 GlyArgAspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 176
 Db 1101 GGAAGAGATTCATCCGTCAGTTCAAGCAGATTACCTCATCTTCAAGAGCTGTA 1160
 QY 177 -----TrrAspPro 179
 Db 1161 TCCACATCAGACGCCGAGAGATGAATGACAGATCATCAATTTCATTTTGAACCT 1220
 QY 180 TrpGluGlu---ProGluAspAla-----AlaProValAlaProSerValPro 194
 Db 1221 GGAAGAGACATTCAGAAAGTCAATCATGATGAATATCTCTGTGATTAATGCGCGGTG 1280
 QY 195 AlaSerGlyTrpProGlu-----LeuProThr 203
 Db 1281 GAATGGGCTTTAGTAAAGCTGTAAACAAGACAGATTTCAGAGAAATCTTAGCAACT 1340
 QY 204 Pro----- 204
 Db 1341 GGAAGAAATTATAGACTAGTCAATGATCTTGTGTAGACTTCAATGACAGAAAGTAA 1400
 QY 205 ---ArgArgGluValGlnSerGlnSerAlaGlnGlnProGlyValIleArgAsp----- 220
 Db 1401 ATTAAGGAG 1460
 QY 220 ----- 220
 Db 1461 ATCCGAGAAATATAGATGACATTTTCAACATTTGATGATTAATCCATCTGAT 1520

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QY 220 ----- 220
Db 1521 AGTCTACTAATGCGGAATTATTAATGACAAAGACATGATTATTAAACAGAGACA 1580
QY 220 ----- 220
Db 1581 CAGACGCTTTTCAAGCAAGAACTGATGATGATTTAGTAAAGAAATATTGCA 1640
QY 220 ----- 220
Db 1641 GCCACTGATTTCAGAACTCTCTGCAAGAGCTGAAGCTGTTATATGACATTATT 1700
QY 221 ----- 221
Db 1701 GTGCAACAGACATTAATATATTTCCACAGAGATGTTTCAGATCTACAGTGGAGAA 1760
QY 224 GlnLeuArgArgLeuGlnGlnGlnArgThrCysLeuAspArgAlaValSer 243
Db 1761 CAATTGCGAGACTACAAAGAAAGAAACATGTAAGTGTATGACAAAGAGTGTCC 1820
QY 244 IleValPheValProCysGlyHisLeu---ValCysAlaGluCysAlaProGlyLeuGln 262
Db 1821 ATAGGTTTATTCTTGTGTGTCATCTAGTATGCAAAAGATTGTCTCTTTCTTAAGA 1880
QY 263 LeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 1881 AAGTGCTCTATTGTAGAGATCAATCAAGGTCACAGTTCGTACATTTCTTTCA 1934

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RESULT 9

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US-08-569-749-3
: Sequence 3, Application US/08569749
: Patent No. 6187557
: GENERAL INFORMATION:
: APPLICANT: Roche, Mike
: APPLICANT: Goeddel, David V
: TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/569,749
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Brezner, David J.
: REGISTRATION NUMBER: 24,774
: REFERENCE/DOCKET NUMBER: A-62464/DBJ
: TELEPHONE: (415)781-1989
: TELEFAX: (415)398-3249
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2601 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-569-749-3

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Alignment Scores:

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Pred. No.: 1.15e-30 Length: 2601
Score: 472.00 Matches: 118

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Percent Similarity: 37.7% Conservative: 47
Best Local Similarity: 26.9% Mismatches: 85
Query Match: 27.4% Indels: 188
DB: 3 Gaps: 11
US-09-762-577B-12 (1-309) x US-08-569-749-3 (1-2601)

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QY 1 MetGlyProIlePheSerAlaValCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 711 ATAGACCTCGAGACAGAGTGGCTTGCTTGGCTGGTGGAGAAATAGACATTTGGGAA 770
QY 21 AlaGlyAspGlyProThrGlnGlu---ArgCysGlyProArgSerLeuGlySerPro 38
Db 771 CCGAAGATTAATGCTATGTCAGAAACCTGAGACATTTTCCAAA----- 815
QY 39 ValLeuGlyLeuAspThrCysArgAlaTrpPheHisValAspGlyGlnIleLeuGlyGln 58
Db 816 -----TGC----- 818
QY 59 LeuArgProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 78
Db 819 -----CAATTATGAAATCAGCTTCAGACACTTCAGATACACAGTTCTTAAT--- 869
QY 79 ProAlaPheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheThrAspTrpPro 98
Db 870 -----CTGAGCATGACACATGACATGACCGCCCTTAAACATTTCTTAACCTGGCCC 920
QY 99 LeuThrAlaGluValProProGlnLeuAlaAlaAlaGlyPhePheHisThrGlyHis 118
Db 921 TCTAGTGTCTAGTAAATCTGACGACCTTCAAGTGGGTTTATTATGTTGGGTAAAC 980
QY 119 GlnAspIleValArgCysPhePheCysGlyGlyGlnGlnGlnGlnGlnGlnGlnGlnGln 138
Db 981 AGTGATGATGTCAAATGCTTTTCTGTGATGTGACCTGAGTGTGGAAATCTGGAGAT 1040
QY 139 AspProTrpThrGlnHisAlaValSerTrpPheProSerCysGlnPheLeuLeuArgSerIle 158
Db 1041 GATCATGCGGTTCACCAATGCCAAGTGGTTTCCAGAGTGTGATGATTAAGAAATTA 1100
QY 159 GlyArgAspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySer----- 176
Db 1101 GGACAGAGTTCAATCCGTCAGATTCAGCCGTTACCTCATCTTGAACACGCTGCTA 1160
QY 177 -----TrpAspPro 179
Db 1161 TCCACATCAGACACGCCAGAGATGAATAATGACAGTCATCATTTGCAACT 1220
QY 180 TrpGlnGlu---ProGluAspAla-----AlaProValAlaProSerValPro 194
Db 1221 GGAGAGACCATTCAGAAAGATGCAATCATGATGAATATCTCTGTGATTANGTGCGCGTG 1280
QY 195 AlaSerGlyTrpProGlu-----LeuProThr 203
Db 1281 GAATGGCTTTTACTAGAACCTGTGTAAACAGACAGTTTCAGAGAAATCTTAGCAACT 1340
QY 204 Pro----- 204
Db 1341 GGAGAGATTAATAGACTAGTCATGATCTTGTGTAGACTTACTCAATGACAGAAATGAA 1400
QY 205 ---ArgArgIleValGlnSerGluSerAlaGlnGluProGlyAlaArgAsp----- 220
Db 1401 ATAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1460
QY 220 ----- 220
Db 1461 ATCCGGAAGATAGAAATGAGCATTTTTCACATTGACCTTGTTAATTCGAATCTGGAT 1520
QY 220 ----- 220
Db 1521 AGTCTACTAATGCGGAATTATTAATGAAACAAAGACATGATTATTAAACAGAGACA 1580
QY 220 ----- 220

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Db 1641 GCCACTGATTCAGAAACTCTCTGCAGAGAGCTGAGCTGTATATAGCATTTATTT 1700
QY 221 -----ValGluA 223
Db 1701 GTGCAACAGACATAAAATATATTTCCTCCACAGAGATGTTTACATTCACAGAGAA 1760
QY 224 GlnLeuAArgArgLeuGlnGlnGlnArgThrCysIysValCysLeuAspArgAlaValSer 243
Db 1761 CAATTGCCGAGCTACAGAGAAAGACATGTAAAGTGTATGACAAAGAGTGTCC 1820
QY 244 IleValPheValProCysGlyIleLeu---ValCysAlaGluCysAlaProGlyLeuGln 262
Db 1821 ATAGGTTTATCTCTGTGTCATCTAGTATGACAAAGATGTGCTCTCTTTAAGA 1880
QY 263 LeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 1881 AAGGTCTCTATTGTAGAGATCAATCAAGGCTACAGTTCTGACATTTCTTTCA 1934

RESULT 11

US-10-232-286-3

Sequence 3, Application US/10232286

Patent No. 6855815

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

TITLE OF INVENTION: David V

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/232,286

FILING DATE: 30-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2601 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-232-286-3

Alignment Scores:

Pred. No.: 1,15e-30 Length: 2601
Score: 472.00 Matches: 118
Percent Similarity: 37.7% Conservative: 47
Best Local Similarity: 26.9% Mismatches: 85
Query Match: 27.4% Indels: 188
DB: 3 Gaps: 11

US-09-762-577B-12 (1-309) x US-10-232-286-3 (1-2601)

QY 1 MetGlyProIleuAspSerAlaIysCysLeuHnIAsrGlyProGlnProSerHnIAla 20
Db 711 ATAGAACCTTGAGACAGAGTGGCTTGCTTGCTGCTGGTGAATAATGACATTTGGAA 770
QY 21 AlaGlyAspGlyProThrGlnGlu-----ArgCysGlyProArgSerLeuIysPro 38
Db 771 CCAGAGATTAATGCTATGTCAGAACCTTGAGACATTTCCGAAA----- 815
QY 39 ValLeuGlyLeuAspThrCysArgAlaIlePheAsnIleValAspGlyGlnIleuGln 58
Db 816 -----TGC----- 818
QY 59 LeuArgProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 78
Db 819 -----CAATTTATAGAAATACAGCTTCAAGACCTTCAAGATACAGATTTCTAT-- 869
QY 79 ProAlaPheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 98
Db 870 -----CTGAGCATGACAGACACATGACGCCCTTTAAACATTTCTTAACCTGCC 920
QY 99 LeuThrAlaGluValProProGlyLeuLeuAlaAlaAlaGlyPhePheHnIThrGlyHs 118
Db 921 TCTAGTGTCTAGTTAATCTGACGACCTTGACAGCTTGACAGCTGTTTATATGCGTAC 980
QY 119 GlnAspIysValArgCysPhePhePheCysGlyGlyGlnGlnGlnGlnGlnGlnGln 138
Db 981 AGTGAATGATGTCACAAAGCTTGTCTGTATGAGTGTGACAGGTGTGGAAATCTGAGAT 1040
QY 139 AspProTrpThrGlnHnIAlaIysTrpPheProSerCysGlnPheLeuIysSerIys 158
Db 1041 GATTCATGGGTTCACATGACATGACAGGTGTTCCAGGTGTGAGTCTGATAGATTTAA 1100
QY 159 GlyArgAspPheValHnIserValGlnGlnHnIAsrGlnLeuGlySer----- 176
Db 1101 GACACAGAGTTATCTGTCAGAGTTACACCCAGTTACCTTACTTAAACAGCTGCTA 1160
QY 177 -----TTPAspPro 179
Db 1161 TCCACATGACAGCCGACGAGATGAAATGACAGTTCATCAATTCATTCATTCATTC 1220
QY 180 TrpGluGlu---ProGlnAspAla-----AlaProValAlaProSerValPro 194
Db 1221 GAGAGAGACCATTCAGAGATGACATGATGAATACTCTGTGATTAATGCGCGTG 1280
QY 195 AlaSerGlyTrpProGlu-----LeuProThr 203
Db 1281 GAATGGGCTTTAGTAGAAGCTGTAAACAGACAGTTACAGAGAAAATCTTAGCACT 1340
QY 204 Pro----- 204
Db 1341 GAGAGAAATTATAGACTAGTCAATGATCTTGTGTAGACTTACTCAATGACAGAAATGAA 1400
QY 205 ---ArgArgGluValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp----- 220
Db 1401 ATAAGGAG 1460
QY 220 ----- 220
Db 1461 ATCCGAGAAATAGAAATGACACTTTTCAACATTTGACTGTGTAAATCCAAATCTGGAT 1520
QY 220 ----- 220
Db 1521 AGTCTAACTGCGGGAATTTATATGACAGAGACATGATGTATTAAACAGAGAGACA 1580
QY 220 ----- 220
Db 1581 CAGAGCTTTTACAG 1640
QY 220 ----- 220
Db 1641 GCCACTGATTCAGAAACTCTCTGCAGAGAGCTGAGCTGTATATAGCATTTATTT 1700

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QY 221 -----ValGluA 223
DB 1701 GTGCACACGACATATAATATATTCCACAGAAAGTGTTCAGATCTTCCAGTGGAGAA 1760
QY 224 GlnLeuAArgIeGluGluGluArgThrCysIysValCysLeuAspArgAlaValSer 243
DB 1761 CATTTGGGAGACTACAAAGAAAGAAACATCTTAAGTGTGATGAGCAAAAGAGTGTCC 1820
QY 244 IleValPheValProCysGlyHisIleu---ValCysAlaGluCysAlaProGlyLeuGln 262
DB 1821 AATAGGTATTAATCTTGTCGTCTAGTACAGTATGCAAAAGTGTGCTCTCTTTAAGA 1880
QY 263 LeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
DB 1881 AAGTGTCTATTGTGAGAGTACAAATCAAGGAGTACAGTTCGTAATTCCTTTCA 1934

RESULT 12
PCT-US96-12860-3
; Sequence 3, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US96-12860-3

Alignment Scores:
Pred. No.: 1,15e-30 Length: 2601
Score: 472.00 Matches: 118
Percent Similarity: 37.7% Conservative: 47
Best Local Similarity: 26.9% Mismatches: 85
Query Match: 27.4% Indels: 188
DB: Gaps: 11

US-09-762-577B-12 (1-309) x PCT-US96-12860-3 (1-2601)
QY 1 MetGlyProIysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 711 ATAGGACCTGGAGACAGAGTGGCTTGTCTTGCCTGTGTGAGAAATTTGAGCAATTTGGGAA 770
QY 21 AlaGlyAspGlyProThrGlnGlu-----ArgCysGlyProAlaGlySerLeuGlySerPro 38

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Db	771	CCGAAGGATTAATGCTATGTCAGAAACACCTGGAACATTTTCCAAA-----	815
Qy	39	ValLeuGIyleuAspThrCysaRgaLatrpAspHisValaSpGIyGlnIleuGIyGln	58
Db	816	-----TGC-----	818
Qy	59	LeuArgProLeuThrGIuGIuGIuGIuGIuGIuGIyAlaGIyAlaThrLeuSerArgIy	78
Db	819	-----CCATTTATAGAAAATCAGCTTCAGACCTTCACMGATACAGACTTTCTAT---	869
Qy	79	ProAlaPheProGIyMeGIySerGIuGIuLeuArgLeuAlaSerPheTryrAspTrpPro	98
Db	870	-----CTGAGCATGCGACACATGCAAGCCCGCTTTAAACATCTTTAACTGGCCC	920
Qy	99	LeuThrAlaGIuValProProGIuLeuLeuAlaAlaAGIyPhePheHisThrGIyHis	118
Db	921	-----TCTACTGTTCTAGTTATATCTGAGCAGCTTCGAATGGCGGTTTTTATATGCGGTAA	980
Qy	119	GlnAspIyValaArgCysPhePheCysTryGIyGIyLeuGlnSerTrpIyAspGIyAsp	138
Db	981	AGTGTGTGTGTCAAAATGCTTTTGTGCTGTATGTGTGATCAGAGTGTGGGAAATCTGAGAT	1044
Qy	139	AspProTrpThrGlnHisAlaIaIystrPhePheProSerCysGlnPheLeuLeuArgSerIyS	158
Db	1041	GATTCATGGGTTTCAACATGCGCAAGTGGTTTTCCAAAGGTGTAGTACTGTGATTAAGATTAA	1100
Qy	159	GIyArgAspPheValHisSerValGIuGIuThrHisSerGlnLeuLeuGIySer-----	176
Db	1101	GGACGAGAGTTTCATCCGTCAGTTCAAGCCAGTTACCTCATCTTCAACAGCTGCTTA	1160
Qy	177	-----TrpAspPro	179
Db	1161	TCCACATCAGACAGCCCGCAGATGAAATGCAAGATCATCATATTCATTTGAACCT	1220
Qy	180	TrpGIuGIu-----ProGIuAspAla-----AlaProValAlaProSerValPro	194
Db	1221	GGAGAAAGCAATTCAGAAAGATGCATCATCATGATGAATACTCTGTGATTAATGCTCCCGTG	1280
Qy	195	AlaSerGIyTryrProGIu-----LeuProThr	203
Db	1291	GAAATGGGCTTTAGTAAAGAGCTGTAAACAGACATTCAGAGAAAAATCTTAGCAACT	1340
Qy	204	Pro-----	204
Db	1341	GGAGAGATTAATAGCTAGTCATGATCTTGTTGTTAGACTTATCTCAATGCAAGATGAA	1400
Qy	205	---ArgArgGIuValGlnSerGIuSerAlaGlnGIuProGIyAlaArgAsp-----	220
Db	1401	ATTAAGGAAGAGAGAGAGAAAGAACATGAGGAAAAAGATCAATGAATTTATTAATTA	1460
Qy	220	-----	220
Db	1461	ATCCGGAAAGATAGAAATGACACTTTTTCACATTTTGACTTGTTGTAATTCCAATCTCGAT	1520
Qy	220	-----	220
Db	1521	AGTCTACTAATCTGCGGATTAATTAATGAACAAGAACATGATGTATTAAACAGAAACA	1580
Qy	220	-----	220
Db	1561	CAGAGCTTTTACAAGCAAGAAACGTGATGTATACATTTTATGTAAGAAATATTTGCA	1640
Qy	220	-----	220
Db	1641	GCCACTGTATTCAGAAACTCTCTGCAAGAACTGAAGCTGTGTATATAGACATTTATTT	1700
Qy	221	-----ValGIuAla	223
Db	1701	GTGCAACAGCATTAATAATATATATTCGCCAGAAAGATTTTCAGATCTTACCGATGGAAGA	1760
Qy	224	GlnIleuArgArgLeuGlnGIuGIuArgThrCysIySerValCysLeuAspArgAlaValSer	243

Db 1761 CAATTGGGAGACTACAAAGAAAGAAATGTAAGTGTATGACAAAGAGTCC 1820
Qy 244 ILevalPhevalProCySeGlyYHISLeu---ValCySaAlaGluCySaAlaProGlyLeuGln 262
Db 1821 ATAGGTTTATTCCTTGGTGCATCTTACTAGTATGCAAGATGGTGCCTCTTTTAA 1880
Qy 263 LeuCyProIleCySaAlaProValArgSerArgValArgThrPheLeuSer 280
Db 1881 AAGTGCTATTGTGAGTACATCAAGGTAAGGTTACAGTTCTGATCATTTCTTCA 1934
RESULT 13
US-09-205-144-1
Sequence 1, Application US/09205144
Patent No. 5958771
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESS
FILE REFERENCE: RUS-0021
CURRENT APPLICATION NUMBER: US/09/205,144
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 3076
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (725)..(2539)
US-09-205-144-1
Alignment Scores:
Pred. No.: 1,44e-30 Length: 3076
Score: 472.00 Matches: 118
Percent Similarity: 37.7% Conservative: 47
Best Local Similarity: 26.9% Mismatches: 85
Query Match: 27.4% Indels: 188
Gaps: 11
US-09-762-577b-12 (1-309) x US-09-205-144-1 (1-3076)
Qy 1 MetGlyProLysAspSerAlaLysCyLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 1313 ATAGGACTGGAAGACAGAGGCTTGGCTTGGCTGGTGGTGAATAATGGCAATGGGAA 1372
Qy 21 AlaGlyAspGlyProThrGlnGlu---ArgCySeGlyProArgSerLeuGlySerPro 38
Db 1373 CCGAAGGATATATGCTATGTCAGAAACCTGAGACATTTCCCAA----- 1417
Qy 39 ValLeuGlyLeuAspThrCySaAlaTrpAspHisValAspGlyGlnLeuGlyGln 58
Db 1418 -----TGC----- 1420
Qy 59 LeuArgProLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 78
Db 1421 -----CAATTATATAAAATCAAGCTTCAAGACACTTCAAGATCAAGCTTTCTAAT--- 1471
Qy 79 ProAlaPheProGlyLysGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpPro 98
Db 1472 -----CTGAGCATGACAGACACATGCAGCCCGCTTAAACATTTCTTAACGGGCC 1522
Qy 99 LeuThrAlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHis 118
Db 1523 TCTAGGCTTCTAGTATATCTTGAAGAGCTTGGCAAGTGGCGGTTTATTATATGCGGTAA 1582
Qy 119 GlnAspLysValArgCySaPhePheCySaTyrGlyGlyLeuGlnSerTrpLysArgGlyAsp 138
Db 1583 AGTGATGATGTCAAATGCTTTTGGTGTATGCTGTGATGCTGAGTCTTGGGAATCTGGAGAT 1642
Qy 139 AspProTrpThrGluHisAlaLysTrpPheProSerCySeGlnPheLeuLeuArgSerLys 158
Db 1643 GATCATGGGTTCACATGCGCAAGTGGTTCCAAAGTGTGAGTACTTGATTAAGATTAA 1702

Qy 159 GlnAspAspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySer----- 176
Db 1703 GGACAGAGTTCATCCGTCATCAAGTTCAGCCAGTTACCCCTCATCTTGAACAGTGGCTA 1762
Qy 177 -----TTPAspPro 179
Db 1763 TCCCATCGACAGCCCGAGAGATGAAAATGACAGTCAATTAATTCATTTGAACCT 1822
Qy 180 TrpGluGlu---ProGluAspAla-----AlaProValAlaProSerValPro 194
Db 1823 GGAGAAGACCATTCAGAAAGATGCAATCATGATGATCTCCGTGATTAATGCTCCGCTG 1882
Qy 195 AlaSerGlyTyrProGlu-----LeuProThr 203
Db 1883 GAATGGCTTATGTAAGACCTGTGTAACAGACAGTTCAAAGAAAATCTTAGCAACT 1942
Qy 204 Pro----- 204
Db 1943 GGAAGAAATTATAGACTAGTCAATGATCTTGTGTAGACTTACTCATATGCAAGAAATGAA 2002
Qy 205 ---ArgArgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp----- 220
Db 2003 ATAAAGGAAAGAGAGAGAAAGAAAGACACTGAGGAAAAGATCAATGATTTATTA 2062
Qy 220 ----- 220
Db 2063 ATCCGAAAGAAATGAAATGCACTTTTTCACATTTGACTGTGTAAATTCACATCTGGAT 2122
Qy 220 ----- 220
Db 2123 AGTCTACTAGTGGCGGAATTATTATGAAACAAGACATGATGTTATTAACAGAGACAA 2182
Qy 220 ----- 220
Db 2183 CAGAGCTTTTAAACAAGAGAAAGAACTGATGATGATGATTTAGTAAAGAAATATTGCA 2242
Qy 220 ----- 220
Db 2243 GCCACTGATTCAGAAACTCTCTGCAAGAAAGCTGAGCTGTGTATATGACATTTATTT 2302
Qy 221 -----ValGluAla 223
Db 2303 GTGCAACAGACATATAAATATATTTCCACAGAGATGTTCAAGATCTTACACAGTGGAA 2362
Qy 224 GlnLeuArgArgLeuGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 243
Db 2363 CAATTGGGAGACTACAAAGAAAGAAAGAAATGTAAGTGTGTATGCAAAAGAAAGTCTCC 2422
Qy 244 ILevalPheValProCySeGlyHisLeu---ValCySaAlaGluCySaAlaProGlyLeuGln 262
Db 2423 ATAGTGTATTATCTCTTGTGTCATCTAGTATGCAAGATTTGCTCTCTTTTAAAG 2482
Qy 263 LeuCyProIleCySaAlaProValArgSerArgValArgThrPheLeuSer 280
Db 2483 AAGTGCTATTGTGAGAGTACATCAATCAAGGTAAGGTTGCTGATCATTTCTTCA 2536
RESULT 14
US-09-814-915A-11
Sequence 11, Application US/09814915A
Patent No. 6750015
GENERAL INFORMATION:
APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
TITLE OF INVENTION: Thereeto
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1

SEQ ID NO 11
 LENGTH: 3076
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-814-915A-11

Alignment Scores:

Pred. No.: 1,44e-30 Length: 3076
 Score: 472.00 Matches: 118
 Percent Similarity: 37.7% Conservative: 47
 Best Local Similarity: 26.9% Mismatches: 85
 Query Match: 27.4% Indels: 188
 DB: 3 Gaps: 11

US-09-762-577B-12 (1-309) x US-09-814-915A-11 (1-3076)

Qy 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
 Db 1313 ATAGGACCTGGAGACAGAGTGGCTTGGCTTGGCTGGTGGAAATGAGCAATGGGAA 1372
 Qy 21 AlaGlyAspGlyProThrGlnGlu-----ArgCysGlyProArgSerLeuGlySerPro 38
 Db 1373 CCGAAGATATATGCTATGTCTGAGAACACCTGGAGACATTTCCCAA----- 1417
 Qy 39 ValLeuGlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGln 58
 Db 1418 -----TGC----- 1420
 Qy 59 LeuArgProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGln 78
 Db 1421 -----CCATTATAGAAATCAGCTTCACAGACATTCAGATACAGAGTTCTTAAT 1471
 Qy 79 ProAlaPheProGlyMetGlySerGlnGluGlnGluGlnGluGlnGluGlnGluGlnGlu 98
 Db 1472 -----CTGACGATGACAGACAGATGACAGCCCGCTTAAATCTTAACTGGCCC 1522
 Qy 99 LeuThrAlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHis 118
 Db 1523 TCTAGTGTCTAGTTAATCTGAGACGCTTGCAGAGTGGCTTTTATATGCTGTAAC 1582
 Qy 119 GlnAspIlyValAlaGlyCysPhePheCysTyrGlyGlyLeuGlnSerTrpIlyAspGlyAsp 138
 Db 1583 AGTATATATGTCGAATGCTTTTGTCTGATGCTGAGTCTGAGTGTGGAAATCGAGAT 1642
 Qy 139 AspProTrpThrGlnHisAlaIleValTrpPheProSerCysGlnPheLeuLeuAspSerIle 158
 Db 1643 GATCCATGGCTTCAACATGCCAAGTGGTTTCCAGGTGTGAGTACTTGATTAAGATTAA 1702
 Qy 159 GlyArgAspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySer----- 176
 Db 1703 GGACAGAGATTCAATCGTCAAGTTCAAGCCAGTTACCTCATCTTGAACAGCTGCTA 1762
 Qy 177 -----TTPAspPro 179
 Db 1763 TCCACATCAGACAGCCAGAGATGAATAATGACAGTCAATATTCATTTGAACCT 1822
 Qy 180 TrpGluGlu---ProGluAspAla-----AlaProValAlaProSerValPro 194
 Db 1823 GGAAGACACATTCAGAAAGATGATCATATGTAATCTCTGTGATTAATGCTGCCGTG 1882
 Qy 195 AlaSerGlyTyrProGlu-----LeuProThr 203
 Db 1883 GAATGGGCTTTAGTAAAGCTGTAAACAGACAGCTTCAGAAAGAAATCTTAGCACT 1942
 Qy 204 Pro----- 204
 Db 1943 GGAGAGATTATAGACTAGTCAATGATCTTGTAGACTTAATCAATGACAGAAATGA 2002
 Qy 205 ---ArgArgGluValInsSerGluSerAlaGlnGluProGlyAlaAsp----- 220
 Db 2003 ATAAAGGAAGGAGAGAGAAAGCACTGAGGAAAGAAATCAATGATTTATTTATTA 2062
 Qy 220 ----- 220

Db 2063 ATCCGAAAGATAGATGACATTTTCAACATTTGACTTGTGTATTCATTCATCCGTGAT 2122
 Qy 220 ----- 220
 Db 2123 AGTCTACTAATGCGGAAATTAATTAATGAACAGAAATGATGTTATTAACAGAGACA 2182
 Qy 220 ----- 220
 Db 2183 CAGAGCTTTACAGCAGAGAACTGATGATTCATTTAGTAAAGAAATATTGCA 2242
 Qy 220 ----- 220
 Db 2243 GCCAGTATTACAGAACTCTGCAAGAGCTGAGCTGTGTTATAGCAATTAATTT 2302
 Qy 221 -----ValGluAla 223
 Db 2303 GTGCACAGACATTAATATATATTCACAGAAAGATTTACAGATTCACAGGAGAA 2362
 Qy 224 GlnLeuArgArgLeuGlnGlnGluArgThrCysIleValCysLeuAspArgAlaValSer 243
 Db 2363 CAATTGGGAGACTTACAGAAAGAAAGACATGTAAAGTGTGTGACAAAGAGTCTC 2422
 Qy 244 IleValPheValProCysGlyHisIleu---ValCysAlaGluCysAlaProGlyLeuGln 262
 Db 2423 ATAGTGTATTATCTTGTGTGTCATCTAGTATGAGTAAGAAATGTGCTCTTCTTAA 2482
 Qy 263 LeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 Db 2483 AAGTGTCTTATTTGTAGAGTACATCAAGGATGACAGTTGTGATCATTTCTTCA 2536

RESULT 15
 US-09-949-016-160
 Sequence 160, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTUR, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 160
 LENGTH: 3165
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-160

Alignment Scores:
 Pred. No.: 1.5e-30 Length: 3165
 Score: 472.00 Matches: 118
 Percent Similarity: 37.7% Conservative: 47
 Best Local Similarity: 26.9% Mismatches: 85
 Query Match: 27.4% Indels: 188
 DB: 3 Gaps: 11

US-09-762-577B-12 (1-309) x US-09-949-016-160 (1-3165)

Qy 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
 Db 1313 ATAGGACCTGGAGACAGAGTGGCTTGGCTTGGCTGGTGGAAATGAGCAATGGGAA 1372
 Qy 21 AlaGlyAspGlyProThrGlnGlu-----ArgCysGlyProArgSerLeuGlySerPro 38
 Db 1373 CCGAAGATATATGCTATGTCTGAGAACACCTGGAGACATTTCCCAA----- 1417

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2006, 21:23:14 ; Search time 906 Seconds
(without alignments)
2820.351 Million cell updates/sec

Title: US-09-762-577B-12
Perfect score: 1721
Sequence: 1 MGPKDSAKCLHRGPDSHMA.....GLOSGLPAPLPLFTWFMAC 309

Scoring table:
BLOSUMP62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/abs/ABSSMBR.spool/US09762577/runat_19042006_111140_25027/app_query.fasta_1
-DB=Published Applications_NA_Main -OPT=fastcap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosump62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR.SCORE=pct
-THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h
-USER=US09762577@CCN_1_1.1026@runat_19042006_111140_25027 -NCPU=6 -ICPU=3
-NO MAP -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=6 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications_NA_Main.*

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9: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1713	99.5	1260	US-10-188-646-4	Sequence 4, Appl1
2	1713	99.5	1268	US-10-807-897-28	Sequence 28, Appl1
3	1713	99.5	1376	US-10-244-586-1	Sequence 1, Appl1
4	1694	98.4	1168	US-10-188-646-12	Sequence 12, Appl1
5	1694	98.4	1322	US-10-807-897-26	Sequence 26, Appl1
6	1694	98.4	1337	US-10-235-026-1	Sequence 1, Appl1
7	1694	98.4	1363	US-10-839-882-37	Sequence 37, Appl1

8	1547	89.9	843	US-10-244-586-2	Sequence 2, Appl1
9	1489.5	86.5	3782	US-10-450-763-27357	Sequence 27357, A
10	1372.5	79.8	769	US-10-203-708-22	Sequence 22, Appl1
11	1354	78.7	1068	US-10-203-708-21	Sequence 21, Appl1
12	1030	59.8	4810	US-10-188-646-11	Sequence 11, Appl1
13	918.5	53.4	614	US-10-450-763-27354	Sequence 27354, A
14	914.5	53.1	615	US-10-296-115-63	Sequence 63, Appl1
15	867	50.4	858	US-10-723-860-8265	Sequence 8265, Ap
16	846	49.2	449	US-10-723-860-4697	Sequence 4697, Ap
17	791.5	46.0	676	US-10-723-860-4448	Sequence 4448, Ap
18	571	33.2	339	US-10-983-995-1	Sequence 1, Appl1
19	478.5	27.8	2673	US-10-482-952-2	Sequence 2, Appl1
20	478.5	27.8	2676	US-09-974-592-11	Sequence 11, Appl1
21	472	27.4	2563	US-10-305-120-1076	Sequence 1076, Ap
22	472	27.4	2563	US-10-641-623-894	Sequence 894, Ap
23	472	27.4	2563	US-10-485-225-63	Sequence 63, Appl1
24	472	27.4	2601	US-10-232-286-3	Sequence 3, Appl1
25	472	27.4	2601	US-10-934-717-3	Sequence 3, Appl1
26	472	27.4	3076	US-09-954-456-1635	Sequence 1635, Ap
27	472	27.4	3076	US-09-954-531-16	Sequence 16, Appl1
28	472	27.4	3076	US-10-197-290-1	Sequence 1, Appl1
29	472	27.4	3076	US-10-388-263-157	Sequence 157, App
30	472	27.4	3076	US-10-776-827-11	Sequence 11, Appl1
31	472	27.4	3076	US-10-843-641A-1083	Sequence 1083, Ap
32	472	27.4	3076	US-10-843-641A-4662	Sequence 4662, Ap
33	472	27.4	3076	US-11-048-271-1	Sequence 1, Appl1
34	472	27.4	3164	US-10-141-618-5	Sequence 5, Appl1
35	472	27.4	3165	US-10-269-909-5	Sequence 5, Appl1
36	472	27.4	3165	US-10-172-118-564	Sequence 564, App
37	472	27.4	3165	US-10-366-307-5	Sequence 5, Appl1
38	472	27.4	3165	US-10-342-887-564	Sequence 564, Appl1
39	472	27.4	5212	US-10-825-282-39	Sequence 39, Appl1
40	472	27.4	5844	US-09-971-392-253	Sequence 253, App
41	472	27.4	5857	US-10-247-671-18	Sequence 18, Appl1
42	472	27.4	6669	US-09-974-592-5	Sequence 5, Appl1
43	472	27.4	6669	US-10-636-065-230	Sequence 230, App
44	465	27.0	1815	US-10-975-974-53	Sequence 53, Appl1
45	465	27.0	2676	US-09-201-936-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-10-188-646-4
; Sequence 4, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: KENNETH W. DOBIE
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1016)
US-10-188-646-4

ALIGNMENT Scores:

Pred. No.: 1.24e-156
Score: 1713.00
Percent Similarity: 99.7%
Best Local Similarity: 99.7%
Query Match: 99.5%
DB: 6
US-09-762-577B-12 (1-309) x US-10-188-646-4 (1-1260)

Length: 1260
Matches: 308
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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QY      1 MetGlyProLyAspSerAlaLeuCySerLeuHisArgGlyProGlnProSerHisTrpAla 20
Db      174 ATGGAGACCTAAAGACAGTGGCCAGAGTCCCTGCACCTGGACCAACAGCCAGCCTGGGCA 233
QY      21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      234 GCCGATGATGGTCCACCCAGAGAGCGCTGTGAGACCCCGCTCTCTGGGAGCCCTGTCCTA 293
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
Db      294 GGCCTGGACACCTGGAGAGCTGGGACCACTGGATGGACAGATCTGGGCGACGCTCGG 353
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY      81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
Db      414 TTCCCGGCAATGGGCTCTGAGAGATGGCTGTGGCTCTCTTAATGACTGGCCGCTGACT 473
QY      101 AlaGlyValProProGlyLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      474 GCTAGAGTGCCACCCGAGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 533
QY      121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      534 AAGGTGAGGTGCTCTCTCTGATGGGGGCTGAGAGCTGGAAGCGCGGAGAGAGAGAG 593
QY      141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db      594 TGGAGGAGATGCGCAAGTGGTCCCAAGCTGTCACTGCTGGCTGGCTGGCTGGCTGG 653
QY      161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db      654 GACTTGTCTCAAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200
Db      714 GAAGAACCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 773
QY      201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
Db      774 CTGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 833
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      834 GTGGAGGCGAGCTGGCGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY      241 AlaValSerIleValPheValProCysGlyHisIleuValCysAlaGlnCysAlaProGly 260
Db      894 GCGGTGTTCATCGTCTTTGTGGCGGTGGCCACCTGGTGTGTGTGTGTGTGTGTGTGT 953
QY      261 LeuGlnLeuCyProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      954 CTGGAGCTGTGGCCCTGTGACAGAGCCCGCTGGAGCGCGGTGGAGCCTTCTGTGCC 1013
QY      281 ***AlaArgCysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCys 300
Db      1014 TAGGCGAGGTGCATAGCGCGGCGAGGTGGCTGGAGAGTGGGCTCCGCCCCCTCTGCG 1073
QY      301 LeuPheTrpThrValPheTrpAlaCys 309
Db      1074 CTGTCTGGACTGTGTCTGGGCTGTGC 1100

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RESULT 2
US-10-807-897-28

; Sequence 28, Application US/10807897

; Publication No. US20040192631A1

; GENERAL INFORMATION:

; APPLICANT: Xiang, Rong

; APPLICANT: Zhou, He

; APPLICANT: Reifeid, Ralph A.

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; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: TSRI-874.1
; CURRENT APPLICATION NUMBER: US/10/807,897
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,009
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 28
; LENGTH: 1268
; TYPE: DNA
; ORGANISM: homo sapiens
; NAME/KEY: CDS
; LOCATION: (174) ... (1016)
; US-10-807-897-28

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Alignment Scores:

Pred. No.:	1,24e-156	Length:	1268
Score:	1713.00	Matches:	308
Percent Similarity:	99.74	Conservative:	0
Best Local Similarity:	99.74	Mismatches:	1
Query Match:	99.54	Indels:	0
DB:	8	Gaps:	0

US-09-762-577b-12 (1-309) x US-10-807-897-28 (1-1268)

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QY      1 MetGlyProLyAspSerAlaLeuCySerLeuHisArgGlyProGlnProSerHisTrpAla 20
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QY      21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      234 GCCGATGATGGTCCACCCAGAGAGCGCTGTGAGACCCCGCTCTCTGGGAGCCCTGTCCTA 293
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
Db      294 GGCCTGGACACCTGGAGAGCTGGGACCACTGGATGGACAGATCTGGGCGACGCTCGG 353
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY      81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
Db      414 TTCCCGGCAATGGGCTCTGAGAGATGGCTGTGGCTCTCTTAATGACTGGCCGCTGACT 473
QY      101 AlaGlyValProProGlyLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      474 GCTAGAGTGCCACCCGAGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 533
QY      121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      534 AAGGTGAGGTGCTCTCTCTGATGGGGGCTGAGAGCTGGAAGCGCGGAGAGAGAGAG 593
QY      141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db      594 TGGAGGAGATGCGCAAGTGGTCCCAAGCTGTCACTGCTGGCTGGCTGGCTGGCTGG 653
QY      161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db      654 GACTTGTCTCAAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200
Db      714 GAAGAACCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 773
QY      201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
Db      774 CTGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 833

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DB: 6 Gaps: 1

US-09-762-577b-12 (1-309) x US-10-188-646-12 (1-1168)

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QY 1 MetGlyProLyAspSerAlaLyCyLeuHiSaArgLyProGlnProSerHiSTrPA1a 20
Db 1 ATGGAGCTTAAGACAGTGCAGAGCTGCACCGTGACACAGCCGACCTGGAGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCySgLyProArgSerLeuGlySerProValLeu 40
Db 61 GCCGGTAGTGTCCACAGCAGAGACCGCTGTGACCCCGCTCTCTGGGAGCCCTGTCTTA 120
QY 41 GlyLeuAspThrCySaGAlaTrpAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
Db 121 GGCTGTGACACCTGCAGAGCTGTGGACCACTGTGATGGAGATCCTGGGGCAGCTGGCG 180
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 241 TTCCCGGAGATGGGCTGTGAGAGAGTTCGCTGTGCTCTTCTATGACTGGCCGCTGACT 300
QY 101 AlaGlnValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 301 GCTAGAGTGCACCCGAGCTGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 121 LyValAlaArgCyPhePheCySTyrgLyGlyLeuGlnSerTrpLyAspArgGlyAspAspPro 140
Db 361 AAGGTGAGTGTCTTCTCTGCTATGGGGGCTGTGACAGCTGTGAGAGCGGGAGAGAGAGAG 420
QY 141 TrpThrGlnHisAlaLySTrPheProSerCySgInPheLeuLeuArgSerLySgLyArg 160
Db 421 TGGACGAGAGATGCAGAGTGTCTCCCAAGCTGTCACTGCTGCTGCTGCTGCTGCTGCTG 480
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db 481 GACTTGTGTCCAGATGTGCAGAGAGACTCTCCAGCTGTGGGCTCTTGGAGCCCGTGG 540
QY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyTrpGln 200
Db 541 GAAGAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGln----- 215
Db 601 CTGCCCAACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 216 -----ProGlyAlaArgAspValGln 222
Db 661 CCAGCCGAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 223 AlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 242
Db 721 GGGAGAGCTCGGGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 243 SerIleValPheValProCySgLyHisIleuValCySaAlaGlnCyAlaProGlyLeuGln 262
Db 781 TCCATGTCTTTGTGCGCGAGCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 263 LeuCyProIleCySaArgAlaProValArgSerArgValArgTrpPheLeuSer**Ala 282
Db 841 CTGTGCCCATGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 283 ArgCyHisGlyArgProGlyGlyLeuGlnSerGlyLeuProIleProLeuCyLeuPhe 302
Db 901 AAGGTGCATGGCCGGGAGAGTGGGCTGTGAGAGTGGGCTGTGAGAGAGAGAGAGAGAGAGAG 960
QY 303 TrpThrValPheTrpAlaCyS 309
Db 961 TGGACTGTGTCTTGGGCGCTGC 981
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RESULT 5

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US-10-807-897-26
/ Sequence 26, Application US/10807897
/ Publication No. US20040192631A1
/ GENERAL INFORMATION:
/ APPLICANT: Xiang, Rong
/ APPLICANT: Zhou, He
/ APPLICANT: Reisfeld, Ralph A.
/ TITLE OF INVENTION: THE SCRIPTS RESEARCH INSTITUTE
/ TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
/ FILE REFERENCE: TSRI-874.1
/ CURRENT APPLICATION NUMBER: US/10/807,897
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/457,009
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq For Windows Version 4.0
/ SEQ ID NO 26
/ LENGTH: 1322
/ TYPE: DNA
/ ORGANISM: homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (174) ... (1070)
/ US-10-807-897-26
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Alignment Scores:

Pred. No.:	9,13e-155	Length:	1322
Score:	1694.00	Matches:	308
Percent Similarity:	94.24	Conservative:	0
Best Local Similarity:	94.24	Mismatches:	1
Query Match:	98.44	Indels:	18
DB:	8	Gaps:	1

US-09-762-577b-12 (1-309) x US-10-807-897-26 (1-1322)

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QY 1 MetGlyProLyAspSerAlaLyCyLeuHiSaArgLyProGlnProSerHiSTrPA1a 20
Db 174 ATGGAGCTTAAGACAGTGCAGAGCTGCACCGTGACACAGCCGACCTGGAGCA 233
QY 21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
Db 224 GCCGTGTGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 293
QY 41 GlyLeuAspThrCySaGAlaTrpAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
Db 294 GGCTGTGACACCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 353
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 414 TTCCCGGAGATGGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 473
QY 101 AlaGlnValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTAGAGTGCACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 533
QY 121 LyValAlaArgCyPhePheCySTyrgLyGlyLeuGlnSerTrpLyAspArgGlyAspAspPro 140
Db 534 AAGGTGAGTGTCTTCTCTGCTATGGGGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 593
QY 141 TrpThrGlnHisAlaLySTrPheProSerCySgInPheLeuLeuArgSerLySgLyArg 160
Db 594 TGGACGAGAGATGCAGAGTGTCTCCAGGTGTCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 653
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db 654 GACTTGTGTCCAGTGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713
QY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyTrpGln 200
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Db 714 GAAGAAACCGGAAAGACGAGCCCTGTGACCCCTCCCTCCCTGCTGAGTACCTGAG 773
Qy 201 LeuProthrProArgrArgLValaGlnSerLuserLagLngu----- 215
Db 774 CTGCCACACCCAGAGAGAGAGTCACTGTAAGTGTCCAGAGAGAGAGAGGAGTCACT 833
Qy 216 -----ProGlyAlaArgAspValGlu 222
Db 834 CCAGCCAGGCGCCAGAGAGGCGTGTGCTTCTTGAACCCCGAGAGAGAGAGATGTGAG 893
Qy 223 AlaGlnLeuArgArgLeuGlnGlnArgThrCysLeuValCysLeuAspArgAlaVal 242
Db 894 GCGCAGCTGCGCGCGCTGACAGAGAGAGAGAGCTGCAAGAGTGTCTGTGACCGCGCTG 953
Qy 243 SerLeuValPheValProCysGlyValLeuValCysAlaGluCysAlaProGlyLeuGln 262
Db 954 TCCATGCTCTTGTGCGGTGCGGCGACCTGTGTGTGAGTGTGCGCGCGCTGACG 1013
Qy 263 LeuCyseProLleCyseArgAlaProValArgSerArgValArgThrPheLeuSer**Ala 282
Db 1014 CTGCGCCCATCTGCAAGAGCCCGCTGCGAGCGCGCTGCGACCTTCTGTCTTACGACC 1073
Qy 283 ArgCysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCysLeuPhe 302
Db 1074 AGGTGCATGAGCGCGCGAGGTGGGCTGCAAGTGGGCTCCCTGCGCTCTGCTGCTTC 1133
Qy 303 TrpThrValPheTrpAlaCys 309
Db 1134 TGGACTGTGTCTGCGGCTGC 1154

RESULT 6

US-10-235-026-1
; Sequence 1, Application US/10235026
; Publication No. US20030082725A1
; GENERAL INFORMATION:
; APPLICANT: Deng, Gang
; APPLICANT: Lin, Jiling-Huey
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: DNA Encoding a No. US20030082725A1el Human Inhibitor-of-Apoptosis
; FILE REFERENCE: 50972AUSD1
; CURRENT APPLICATION NUMBER: US/10/235, 026
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 09/127, 928
; PRIOR FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)..(1066)
; OTHER INFORMATION:
US-10-235-026-1

Alignment Scores:

Pred. No.: 9,24e-155 Length: 1337
Score: 1694.00 Matches: 308
Percent Similarity: 94.2% Conservative: 0
Best Local Similarity: 94.2% Mismatches: 1
Query Match: 98.4% Indels: 18
DB: 5 Gaps: 1

US-09-762-577b-12 (1-309) x US-10-235-026-1 (1-1337)

Qy 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 170 ATGGAGCTTAAGACATGCTCAAGTGCCTGACCGGTGAGACCAAGCCGACCTAGGCA 229
Qy 21 AlaglyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlnSerProValLeu 40

Db 230 GCCGATGATGTGCCCAAGAGAGCGCTGTGACCCCGCTCTGTGGAGACCCCTGTCTTA 289
Qy 41 GilyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLileuGlyGlnLeuArg 60
Db 290 GGCCTGACACCTTGACAGAGCTTGAGACCAAGTGAATGAGAGATCTTGAGCCAGCTGCG 349
Qy 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 350 CCCCTGACAG 409
Qy 81 PheProGlyMetGlySerGlyGlnLeuValLeuValSerPheTrpAspTrpProLeuThr 100
Db 410 TTCCTCCGAGTGTGCTCTGAGAGTGTGCTGCTGCTGCTCTCTATGATCTGCGCTGACT 469
Qy 101 AlaGluValProProGlyLeuLeuValAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 470 GCTGAGGTGCACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 529
Qy 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db 530 AAGTGAAGTGTCTTCTTCTGCTATGAGGAGCTGCAAGAGAGAGAGAGAGAGAGAGAG 589
Qy 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 590 TGGACGAGAGCATGCCAAGTGTGCTCCAGAGCTGTCAAGTCTGCTGCTGCTGCTGCTGCT 649
Qy 161 AspPheValHisSerValGlnGlnTrpHisSerGlyLeuLeuGlySerTrpAspProTrp 180
Db 650 GACTTGTGTCCAGAGTGTGACAGAGACTCACTCCAGCTGTGTGAGCTTGTGAGACCGCTG 709
Qy 181 GlnGlnProGlyLysAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db 710 GAAGAAACCGAAGACAG 769
Qy 201 LeuProThrProArgArgGlnValaGlnSerGlyLuserLagLngu----- 215
Db 770 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTGTGCCAGAGAGAGAGAGAGAGTCA 829
Qy 216 -----ProGlyAlaArgAspValGlu 222
Db 830 CCAGCCAGGCGCCAGAGAGGCGGTGTGCTTGTGAGCCCGCCAGAGAGAGAGATGTGAG 889
Qy 223 AlaGlnLeuArgArgLeuGlnGlnArgThrCysLeuValCysLeuAspArgAlaVal 242
Db 890 GCGCAGCTGCGCGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 949
Qy 243 SerLeuValPheValProCysGlyValLeuValCysAlaGluCysAlaProGlyLeuGln 262
Db 950 TCCATGCTCTTGTGCGGTGCGGCGACCTGTGTGTGAGTGTGCGCGCGCTGACG 1009
Qy 263 LeuCyseProLleCyseArgAlaProValArgSerArgValArgThrPheLeuSer**Ala 282
Db 1010 CTGTGCCCATCTGACAG 1069
Qy 283 ArgCysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCysLeuPhe 302
Db 1070 AGGTGCATGAGCGCGCGAGGTGGGCTGCAAGTGGGCTCCCTGCGCTCTGCTGCTTC 1129

RESULT 7

US-10-839-882-37
; Sequence 37, Application US/10839882
; Publication No. US20040203106A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: CORLEY, Neil C.

```

APPLICANT: LAL, Preeti
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.
APPLICANT: JUNG, Yang
APPLICANT: SHIH, Leo L.
TITLE OF INVENTION: PROLIFERATION AND APOPTOSIS RELATED PROTEINS
FILE REFERENCE: PF-0619 PCT
CURRENT APPLICATION NUMBER: US/10/839,882
PRIORITY FILING DATE: 2004-05-05
PRIORITY APPLICATION NUMBER: US/09/807,452
PRIORITY FILING DATE: 2001-04-11
PRIORITY APPLICATION NUMBER: 09/175,737; unassigned, 60/118,559; 09/249,740; unassigned,
60/154,336
PRIORITY FILING DATE: 1998-10-20; 1998-10-20; 1999-02-04; 1999-04-11; 1999-04-11;
1999-04-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL Program
SEQ ID NO 37
LENGTH: 1363
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incycle ID No: 1520835CBI
US-10-839-882-37

```

```

Alignment Scores:
Pred. No.: 9,44e-155 Length: 1363
Score: 1694.00 Matches: 308
Percent Similarity: 94.2% Conservative: 0
Best Local Similarity: 94.2% Mismatches: 1
Query Match: 98.4% Indels: 18
DB: 8 Gaps: 1

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US-09-762-577b-12 (1-309) x US-10-839-882-37 (1-1363)

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QY 1 MetGlyProIyAspSerAlaIySylLeuHsArgGlyProGlnProSerHisTTPAla 20
DB 215 ATGGGGCTTAAAGACATGCGCAAGTGTCTTACCGTGGACACAGCGGACCACTGGGGA 274
QY 21 AlAGlyAspGlyProThrgIngluArgCySgIyProArgSerLeuGlySerProValLeu 40
DB 275 GCCGGTATGATGCTCCACGACGAGCGCGTGTGACCCCGCTCTGGGACGCTGTCTTA 334
QY 41 GlyLeuAspThrCySargAlaTTPAspHisValAspGlyGlnTleuGlyInleuArg 60
DB 335 GGCCTGGACACCTGGACAGCTGGACCAAGTGAATGGGACAGATCTGGGGCAGCTGCGG 394
QY 61 ProleuThrgIngluIngluIngluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
DB 395 CCCCTGACAGAGAGAGAGAGAGAGCGCGCGGCGCACTTGTTCAGGGGGGCTGCGC 454
QY 81 PheProGlyMetCylSerGlyGlyLeuLeuArgLeuAlaSerPheTyrAspTTPProleuThr 100
DB 455 TTCTCCGGGATGGGCTCTGAGAGTGTGCTGCGCTCTCTTATAGACTGGCGGCTGACT 514
QY 101 AlaGlyValProProGlyLeuLeuAlaAlaIySylPhePheHisThrGlyHisGlnAsp 120
DB 515 GCGGAGTGTCCACCCAGAGCTGTGCTGCTGCGGCTTCTTTCACACAGGCGCATGAGAC 574
QY 121 LysValAlaCySargPhePheCySgIyGlyLeuGlnSerTTPLeuArgGlyAspAspPro 140
DB 575 AAGGTGAGGTGCTTCTTCTGCTATGGGGCTGCGAGAGCTGGAACGCGGGGACAGACCC 634
QY 141 TTPThrgInlHisAlaIySylPheProSerCySgIyPheLeuLeuArgSerIySylArg 160
DB 635 TGGACGAGCATGCGCAAGTGTTCCTCCAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 694
QY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTTPAspProTTP 180
DB 695 GACTTGTTCACAGTGTGAGAGACTCACTCCAGCTGTGAGGCTCTGAGGACCCGCTGG 754
QY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200

```

```

DB 755 GAAAGAACCGGAAACACAGCCCTGTGGCCCCCTCCGCTCTGCTGCTGCTGCTGCTGCTGAG 814
QY 201 LeuProThrProArgArgGlyValGlnSerGlySerAlaGlnGlu----- 215
DB 815 CTGCCACACCCAGAGAGAGAGTTCAGTCTGAAAGTCCACAGAGCAGAGAGGCTGACT 874
QY 216 -----ProGlyAlaArgAspValGlu 222
DB 875 CCAGCCGAGGCCAGAGGGCGTGTGGTCTTTAGAGCCCCCAGAGAGCCAGGATGTGGAG 934
QY 223 AlaGlnLeuArgArgLeuGlnGlnGlyValGlnThrCySylValCylLeuAspArgAlaVal 242
DB 935 GCGGACCTCGGGGGGTGGAGAGAGAGAGAGAGAGTGTGCTGACCCGCGCGG 994
QY 243 SerIleValPheValProCySgIyHisLeuValCylAspAlaGluCylAspProGlyLeuGln 262
DB 995 TCCATGCTTGTGTGTGCGGCGGCGCACCTGTGTCTGAGTGTGCTGCTGCTGCTGCTGCTG 1054
QY 263 LeuCySProIleCySargAlaProValArgSerArgValArgThrPheLeuSer**Ala 282
DB 1055 CTGTGCCCATGTGAGAGCCCGCTCCGACGCGCGGCGCACCTTCTGTCTTACGAGC 1114
QY 283 ArgCySHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCyLeuPhe 302
DB 1115 AGTGCACATGCGCGCGCGCGAGTGGCTGAGAGTGGCTTCCCTGCGCTCTGCTGCTGCTTC 1174
QY 303 TTPThrValPheTTPAlaCys 309
DB 1175 TGGACGTGTTCTTGGGCTGCG 1195

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RESULT 8
US-10-244-586-2

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Sequence 2, Application US/10244586
Publication No. US20030087319A1
GENERAL INFORMATION:
APPLICANT: GOMES, BRUCE C.
APPLICANT: KASOF, GARRETT M.
APPLICANT: PROSSER, JUDITH C.
TITLE OF INVENTION: NOVEL PROTEIN
FILE REFERENCE: DB/009901/0270799
CURRENT APPLICATION NUMBER: US/10/244,586
CURRENT FILING DATE: 2002-09-16
PRIORITY FILING DATE: 2000-06-14
PRIORITY APPLICATION NUMBER: 60/139,291
PRIORITY FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 843
TYPE: DNA
ORGANISM: Homo sapiens
US-10-244-586-2

```

```

Alignment Scores:
Pred. No.: 1.09e-140 Length: 843
Score: 1547.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 89.9% Indels: 0
DB: 5 Gaps: 0

```

US-09-762-577b-12 (1-309) x US-10-244-586-2 (1-843)

```

QY 1 MetGlyProIyAspSerAlaIySylLeuHsArgGlyProGlnProSerHisTTPAla 20
DB 1 ATGGGACCTTAAAGACATGCGCAAGTGTCTTACCGTGGACACAGCGGACCACTGGGGA 60
QY 21 AlAGlyAspGlyProThrgIngluArgCySgIyProArgSerLeuGlySerProValLeu 40
DB 61 GCCGGTATGATGCTCCACGACGAGCGCTGTGAGAGCTTGTGAGGACCCGCTGTGCTTA 120

```

```

Qy 41 GlyLeuAspThrCysAlaGlyAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 121 GGCGTGAACACCTCTCAGAGCTGGGACCACTGGATGGGACATCTGGCCACAGCTGGG 180
Qy 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 81 PheProGlyMetGlySerGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 241 TTCCCGGCGCATGGGCTCTGAGAGTTGGGTCTGGCTCTCTCTATGATGGCCCTGACT 300
Qy 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 301 GCTAGAGGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnIleSerTyrPheAspGlyValAspAspPro 140
Db 361 AAGGTGAGGTGCTCTCTCTCTATGGGGGCTTGCAGAGCTGGAGAGCGGGGAGAGACCC 420
Qy 141 TrpThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 421 TGGACGAGACATGCGCAAGTGTTCCTCCAGCTGTCAATTCCTGCTCCGCTCAAAAGAGA 480
Qy 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db 481 GACTTGTCTCCACAGTGTGACAGAGACCTCACTCCAGCTGCTGGGCTCTGGGACCGGTGG 540
Qy 181 GlnGluProGlnLeuAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db 541 GAAGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 201 LeuProThrProArgTargGlnValGlnSerGlnSerLysGlnGlnGlnGlnGlnGlnGln 220
Db 601 CTGCCCAACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 221 ValGlnAlaGlnLeuArgTargLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 661 GTGAGAGCGGAGCTGGCGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
Db 721 GCCGTGTCAATCTGCTTGTGCGCTGCGGCGCACTGTGTGTGTGTGTGTGTGTGTGTGT 780
Qy 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 781 CTGACGTGTGCTCCCATCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

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OTHER INFORMATION: 95% homologous to Homo sapiens Iyvin inhibitor of-
OTHER INFORMATION: apoptosis, accession number AF311388, Smith-Waterman score=641.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(3782)
OTHER INFORMATION: n = a,t,c or g
US-10-450-763-27357

Alignment Scores:
Pred. No.: 2,1e-134 length: 3782
Score: 1489.50 Matches: 282
Percent Similarity: 75.6% Conservative: 0
Best Local Similarity: 75.6% Mismatches: 3
Query Match: 86.5% Indels: 88
DB: 9 Gaps: 3

US-09-762-577b-12 (1-309) x US-10-450-763-27357 (1-3782)
Qy 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
Db 2200 ATGGGACCTTAAAGACATGTCAGAGTGCCTGTCACCGTGGACACAGCGGACCACTGGGCA 2259
Qy 21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
Db 2260 GCCGATGATGTCTCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2319
Qy 41 GlyLeuAspThrCysAlaGlyAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 2320 GGCTGTGACACCTGCGAGAGCTGGGACACAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAG 2379
Qy 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 2380 CCCCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2439
Qy 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 2440 TTCCCGGCGCATGGGCTCTGAGAGTGTGCTGCTGCTGCTCTCTCTATGATGGCCGTGACT 2499
Qy 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThr 116
Db 2500 GCTGAGGTGCACCCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2559
Qy 116 116
Db 2560 GTGGTCAAGCTGATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 2619
Qy 116 116
Db 2620 AGGCGCCACCGAGAGGCTTAAACAATACCTGACAGAGCATGATTCAGAGAGAGGCT 2679
Qy 117 117
Db 2680 CTGGCGGGGACACCATCTGCGCATTCAGACAGAGTGAAGGTCTTCTTGTGCTATGGGGGC 2739
Qy 131 LeuGlnSerTyrPheArgIleAspAspProTyrThrGlnHisAlaLysTyrPhePro 149
Db 2740 CTGCAAGCTGGAAGAGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2799
Qy 150 150
Db 2800 TACCGGCTGCCCTCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2859
Qy 158 LysGlyValArgAspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTyr 177
Db 2860 AAGAGAGAGACTTGTCTCAGAGTGCAGAGAGACCTCCAGCTGTGGGCTCTCGG 2919
Qy 178 AspProTyrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 197
Db 2920 GACCCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2964
Qy 198 TyrProGlnLeuProThrProArgValGlnSerGlnSerLysGlnGlnGlnGlnGlnGln 217
Db 2965 2965

```


QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
 Db 1 ATGGAGCTTAAGACAGTGCACAGTGCCTGACCGTGCACCAAGCCAGCCACTGGGCA 60
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 Db 61 GCGGGTGAATGCTCCACCGCAGAGGCGCTGTGAGACCCCGCTCTGTGGGAGCCCTGTCTTA 120
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 Db 121 GGCCCTGACACCTGAGAGCTGTGGACCACTGAGATGGGACATCTGGGCGACCTGGCG 180
 QY 61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
 Db 181 CCCCTGACAG 240
 QY 81 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyraSerTrpProLeuThr 100
 Db 241 TTCCCGGCGATGGCTGTGAGAGTGGCTGTGGCTCTCTATGACTGGCCGCTGACT 300
 QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisTrpGlyHisGlnAsp 120
 Db 301 GCTAAGGTGCCACCCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 121 LysValArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
 Db 361 AAGGTGAGTGCTCTCTCTGCTATGGGGCTGTGAGAGCTGGAAGCCGGGAGAGAGAGAG 420
 QY 141 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
 Db 421 TGGACGAGAGCATGCGCAAGTGGTCCCGCAGCTGTGAGTTCCTGCTCCGGTCAAAAGAGA 480
 QY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrp----- 177
 Db 481 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTCTGTGGTGAAGCGCC 540
 QY 177 ----- 177
 Db 541 ACCTCTCTCGGGGCTCCGGGTGGCAGTGGGGTCTGCTCTCTATTTCCCAAGGCT 600
 QY 178 -----AspProTrpGluGluProGluAlaAlaProValAla 190
 Db 601 GATGCTCTGTGCTCTTCCAGAGCCCGTGGAGAAACCGAGAGACCGAGCCCTGTGGC 660
 QY 190 aProSerValPro----- 194
 Db 661 CCCCTCGGTCAGTCTGAAGTGCACGAGCCAGGTGACGCGCGAGACCCCTGGGT 720
 QY 195 -----AlaSerGlyTrpProGluLeuProThrPro----- 204
 Db 721 GAGGAGCTGGGAG 779
 QY 205 -----ArgArgGluVal-----G1 209
 Db 780 GGGCAGAGGTGTGGGACATTTGGCAGGCTGTCTCTAGAGAGGGTCAAGTCCAGCGCA 839
 QY 209 nSerGluSerAla-----GlnGluProGlyAlaArgAspValGlnGluGlnLe 225
 Db 840 GGGCCAGAGGCGGTGGGTCTTGAAGCCCGCAGAGCCAGGAGATGTGAGGGGCGAGCT 899
 QY 225 uArgArgLeuGlnGluArgThrCysLysValCysLeuAspArgAlaValSerIleVal 245
 Db 900 GCGGCGGCTGAG 959
 QY 245 lPheValProCysGlyHisLeuValCysAlaGluCysAlaProGlyLeuGlnLeuCysPr 265
 Db 960 CTTTGTGCTCGGTGGCAGCTGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1019
 QY 265 oLleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 Db 1020 CATCTGAGAGAGCCCGCTCGGACGCGGTGCGACCTTCTGTGCT 1065

RESULT 12
 US-10-188-646-11
 ; Sequence 11, Application US/10188646
 ; Publication No. US20040005565A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Kenneth W. Doble
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
 ; FILE REFERENCE: PRTS-0373
 ; CURRENT APPLICATION NUMBER: US/10/188,646
 ; CURRENT FILING DATE: 2002-07-02
 ; SEQ ID NO 11
 ; LENGTH: 4810
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 US-10-188-646-11
 Alignment Scores:
 Pred. No.: 1 24e-89 Length: 4810
 Score: 1030.00 Matches: 306
 Percent Similarity: 21.7% Conservative: 1
 Best Local Similarity: 21.6% Mismatches: 2
 Query Match: 59.8% Indels: 1107
 DB: 6 Gaps: 6
 US-09-762-577b-12 (1-309) x US-10-188-646-11 (1-4810)
 QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
 Db 310 ATGGAGCTTAAGACAGTGCACAGTGCCTGACCGTGCACCAAGCCAGCCACTGGGCA 369
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 Db 370 GCGGGTGAATGCTCCACCGCAGAGGCGCTGTGAGACCCCGCTCTGTGGGAGCCCTGTCTTA 429
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 Db 430 GGGCTGTGACCTGTGACAGCTGTGAGACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 489
 QY 61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
 Db 490 CCCCTGACAG 549
 QY 81 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyraSerTrpProLeuThr 100
 Db 550 TTCCTCGGATGGGCTGTGAGAGTGTGCTGTGCTCTCTTATGACTGTGCGGCTGACT 609
 QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisTrp----- 116
 Db 610 GCTGAGGTGCAACCGACGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 668
 QY 116 ----- 116
 Db 669 GGGGGGGGGCTTCTCTGCGGTGGGCTGTGGACAGATTCTGACCTTCCAGCCAGAGGC 728
 QY 116 ----- 116
 Db 729 TCTGCTCTCTCGTAGATTCATCCCAAGAGAGAGGTCTGTGGCTGTATGACGAGAGAG 788
 QY 116 ----- 116
 Db 789 TGGTCTGCAAGCCCTCCAGTGCATGGAGCTGTGCTGTGACACCTTCCCGAGTCT 848
 QY 116 ----- 116
 Db 849 CTGCTGCTGAGTGTTCAGACCGTGGAGATGTGAGAGAGGGGCTGCTTGGCCACAGTCT 908
 QY 116 ----- 116
 Db 909 GAGGCTCTAGCTGTGAGAGCGCGCAGCTTGTGTGCAAGTACCTTGTGTATGAGAGT 968

QY 116 ----- 116
Db 969 GGGTGGGCTGACATTGCTGGGGCCCTCACCTTCCCGCTGTGTTCGACAGAGAGA 1028
QY 116 ----- 116
Db 1029 GGAAGTGTTTAAAGACAGGATCAGGGTGACCAAGGAGGAGGTGACAGAGAGTTC 1088
QY 116 ----- 116
Db 1089 CTGATGCTCAGCCTGTGGGGAATTTCTCAAGGCCCACTGACGCTACTGTCTGGTCT 1148
QY 116 ----- 116
Db 1149 TCCCACTGAATCAAGTCCCCGAGTACTATCTTAGTCTTGGCCGGGCTGTCTCTC 1208
QY 116 ----- 116
Db 1209 TGCCCTACAGCTGACGACCATGTGTGACACTTAGTTCAGGTCGCCAGCTCTGCACTTC 1268
QY 116 ----- 116
Db 1269 CTGGCTGAAGGACAGGAGGAGGAGCCACAGAGGCTTTACAAATACGTGGACAGGCAT 1328
QY 116 ----- 116
Db 1329 GGTATTGTCAAGTGGGCTTGGGCGGAGCATTCTGTATAGGCTGAGCAACTTAA 1388
QY 116 ----- 116
Db 1389 GACAGCTGTGGGGGAGCAGTGGCTGGGACGTGACAGAACCGTGGCTGAGAGGGCAGG 1448
QY 116 ----- 116
Db 1449 CCCAGTCACCACCTCCCTGSAAGTCCAAGGCTCAGAGGAGCAAAAGCCAGGAGAGGC 1508
QY 116 ----- 116
Db 1509 ATGGCAGGTGACAGCCGGGGTCTTTGGGGCTGTAGAGGTCCAGTCCCGATGACAGCC 1568
QY 116 ----- 116
Db 1569 AAACCTGTGATGTCAGTGCAGGTGACGTATGCGATGATGCCGATGAGGGAGCGGGTTC 1628
QY 116 ----- 116
Db 1629 GCCAGAGGTAGAGAGATGACGGGTCCCACCCCAAGGAGGATGATTCTAATAA 1688
QY 116 ----- 116
Db 1689 GCAAGCTGGCCCAAGCTGGCTTCTAGAGGAGCCTCCCTTCTTCTCACTGGGAAT 1748
QY 116 ----- 116
Db 1749 CCATCTTGGGAGACAGAGACTGGGAGGGGCCCTTCTGAGCTCTGAAGCCCAAGGCT 1808
QY 116 ----- 116
Db 1809 ATAGATGTACCAAGCCCTGGGGGAGCCCACTGCTCACTTGGAACAATGCAAAATGCCA 1868
QY 116 ----- 116
Db 1869 GCTCAGTCTTCTGTGACATTTCTGCCCATCTGGCCGGACACCAGTCACTTGTTC 1928
QY 116 ----- 116
Db 1929 CCTTTACACTTTGATGCTAATGAGGTACAGTGAATCCCCCAAGAGCCCTTGCCA 1988
QY 116 ----- 116
Db 1989 CCCCCTCTCTCTTTGGCCACTGGAGCTCCCTTCAGCTGAAGTCTCATAGCCTTGG 2048
QY 116 ----- 116

Db 2049 AAGAACACACCGGGGGCCCGGGACTGGGTGGGACTTGGCTGGGAGCAGACTCTCCGC 2108
QY 117 ----- 117
Db 2109 ACCCAGGCCCATCAGGACAAAGGTGAGGTCTTCTGTGCTATGGGGGCTTGAGAGCTGG 2168
QY 135 Iy#AtgGlyAspAspProTThrGluHisAlaLysTTPhePro----- 149
Db 2169 AAGCGGGGAGACGACCCCTGACAGGACATGCCAAGTGGTCCCAAGTACCGGCTGCC 2228
QY 149 ----- 149
Db 2229 CTGGGGGGCCCGGGCTTGATCATAGGTAAGGGGTGGGCCCCCAACGGCTCTGTGACCC 2288
QY 149 ----- 149
Db 2289 AACACAGGCTGTCTTGGCTTCCTGGCCCAAGGACATGGAGAGGCCCTTGTGGG 2348
QY 149 ----- 149
Db 2349 AGGTGCTTGGCCGGCAGGTACCACTTTCTGTGAGGGCCCTTTTGGAAAGGCTG 2408
QY 149 ----- 149
Db 2409 CTGGGGGAGAAATGCTCTCCCATGGGACTTACCTGAAGCCCATGAGAGGCTCTCAC 2468
QY 149 ----- 149
Db 2469 AGCAGCCTCTCGCCATGCCACGAGCACTGCAAGGTGGGAGAGAGGGAGCCCAAC 2528
QY 149 ----- 149
Db 2529 CCTGACCCCGGGATCCAAAGGCTTGAAGACACAGTGGGGGCTTGAAACCCCACTA 2588
QY 150 ----- 150
Db 2589 CATCTCGGGCANTCGACGTGTCAAGTCTGCTCGGGTAAAGAAAGACATTGTTC 2648
QY 164 HisSerValGlnGluThrHisSerGlnLeuLeuLysSerTP----- 177
Db 2649 CACAGTGTGAGAGACTCACTCCAGCTGTGGCTCTGGGTGAGCGCACCTCTCT 2708
QY 177 ----- 177
Db 2709 CGGGGCTCGGGGTGAGTGGGGTCTGCCCTCTCTATTCCCAAGCCTGATGTCTC 2768
QY 178 ----- 178
Db 2769 TGGCTCTTCCAGGACCGGTGGAAAGACGGAAGACGAGCCCTGTGGCCCTCGG 2828
QY 192 ----- 192
Db 2829 TGAAGCTGACACCAACCTGCTGACTCTTGTGCGCTGACGCTGTGGCCAAAG 2888
QY 192 ----- 192
Db 2889 CCACTGGGTGTCCCAACCTCCCAAGACAGAGGAGATGACGGGACGTTGACGGGTCT 2948
QY 192 ----- 192
Db 2949 GACGTGTGCTGTGGTGGCTTCAAGGGGCTGTGCCATGTAGAGGTGGGGGCGGCGG 3008
QY 192 ----- 192
Db 3009 CAGGGGCTCCCAAGTCCAGGCCCCCATTTCTGCTTCTCCAGACTTACCCCTTGGGCA 3068
QY 192 ----- 192
Db 3069 CAGCCATTGCTGTGCAATACCAACCCCAACAGTCCAGACACACAGATCTGACGCT 3128
QY 192 ----- 192

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Db 3129 ACTCCAGATGGGAGATGTGTGACAGAGGACATTGGACAAGGACAGGCTCTGTGTGGCG 3188
QY 192 ----- 192
Db 3189 CCTCCAGAAAGCCTCTGTGATCTGTGTATGTGTGTGGAGAGGGGTGGAGAGAGTGTGGAG 3248
QY 192 ----- 192
Db 3249 CGGGGATACTGTGAGCCCTCTCACTCCGGCCAGAACTGGACCCCAAGGCTGAGACC 3308
QY 192 ----- 192
Db 3309 TGTATCTGGGGCCGGCCAGCTTTCTCTTGGAGTTAGGCTCAAGTCTATCTTAAGTCT 3368
QY 193 -----ValProAlaSerGlyTyrProGluLeuProThrProArgArgGlyValGlnSerGly 211
Db 3369 CCACAGTCCCTGCTCTGTGGTATCCCTGAGTGTGCCACACCCAGAGAGAGGTCCAGTCTG 3428
QY 211 luserAlaGlnGlu----- 215
Db 3429 AAAGTCCCAAGAGCCAGAGTGTGAGGAGCCCGGAGCCCTGTGGTGTGAGGGCTGGGAGG 3488
QY 215 ----- 215
Db 3489 GGGCTGAGAGACCCCGACCTTCCATGAGGAGGTGGGGGCGCAGGGTGTGGAGACA 3548
QY 215 ----- 215
Db 3549 TTTCCAGAGGCTGTCTCTTCTTGAAGGGGTACGTCCAGCCAGGCGCCAGAGGGCGTGTGG 3608
QY 216 -----ProGlyAlaArgAspValGlnValGlnLeuArgArgGlyLeuGlnGlu 231
Db 3609 GTTCTTGAGCCCCCAGAGGAGCCAGGAGATGTGAGGCGCAGCGCGGGCTGTGACAGAGAG 3668
QY 232 ArgThrCysLeuValCysLeuAspArgAlaValSerIleValPheValProCysGlyHis 251
Db 3669 AGGAGGTGTGAGAGGTGTGTGTGAGACCGCGCTGTGACATGCTTGTGTGGCGGTGGCGCAC 3728
QY 252 LeuValCysAlaGluCysAlaPheProGlyLeuGlnLeuCysProIleCysArgAlaProVal 271
Db 3729 CTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3788
QY 272 ArgSerArgValAlaArgThrPheLeu----- 279
Db 3789 CGAGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3848
QY 279 ----- 279
Db 3849 CCAAGCCTCTCTCGAGAGGGGGCCCTGTGAGCGGCTGTGCCGCGCTCTGTGAACCATGCA 3908
QY 279 ----- 279
Db 3909 GGGCTTCCCGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3968
QY 279 ----- 279
Db 3969 CGCCCATCAATCTTACTACCTCCCTTGAACGTTAGTTGGGGGCTGTGTCTGTGGGACAC 4028
QY 279 ----- 279
Db 4029 GTGCCCTGGGCGCCACCATAGTCTGTGCTGTGCTGATTAAGTCAAGCCTGTGGCTCTC 4088
QY 279 ----- 279
Db 4089 TCAGCTTGAATTTTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4148
QY 279 ----- 279
Db 4149 GGGTGGGCGCAGGTTGGGCTTACACAGCAGAGACATGTGGCTGTGACCCGGGGGCA 4208
QY 279 ----- 279
Db 4209 GGCATGTGTGGAAACCTGTGACCGGGAAGGGGGTGTGTGAACCTGTCTTGAAGAGTGGG 4268

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QY 279 ----- 279
Db 4269 TGGGATACCCCAATCTGTGCGGAGGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4328
QY 279 ----- 279
Db 4329 CTGTAGTAACTCCCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4388
QY 279 ----- 279
Db 4389 GGAATCTGGATCTGAGGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4448
QY 280 -----Ser**AlaArgCysHisGlyArgProGlyValGlnSerGlyLeuPro 296
Db 4449 CACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4508
QY 297 AlaProLeuCysLeuPheThrPheValPheThrAlaCys 309
Db 4509 GCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4547

RESULT 13
US-10-450-763-27354
; Sequence 27354, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 27354
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (309)..(614)
; OTHER INFORMATION: 35% homologous to Homo sapiens inhibitor of apoptosis protein
; OTHER INFORMATION: KIAA, accession number AF301009, Smith-Waterman Score=86.
US-10-450-763-27354

Alignment Scores:
Pred. No.: 9,42e-80 Length: 614
Score: 918.50 Matches: 174
Percent Similarity: 87.3% Conservative: 4
Best Local Similarity: 85.3% Mismatches: 6
Query Match: 53.4% Indels: 20
DB: 9 Gaps: 2

US-09-762-577b-12 (1-309) x US-10-450-763-27354 (1-614)
QY 91 LeuAlaSerPheThrAspThrPheProLeuThrAlaGluValProProGluLeuLeuAlaIa 110
Db 5 CTRTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 64
QY 111 AlaGlyPhePheHisThrGlyHisGlnAspLeuValArgCysPhePheCysTyrGlyGly 130
Db 65 GCGGCTCTCTTCCACACAGGCGCATCAGACAAAGTGAAGTGTCTTCTGTGTGTGGGGC 124
QY 131 LeuGlnSerTrpLeuValArgIleAspPheProTrpThrGlnHisAlaIleTrpPheProSer 150
Db 125 CTGCAGAGCTGTGAAGGCGGAGACGACCCCTGTGACGAGACATGCCAAAGTGTCTCCACG 184
QY 151 CysGlnPheLeuLeuArgSerIleGlyArgAspPheValHisSerValGlnGluThrHis 170

```

Db 185 TGTCACTTCCTGCTCCGGTCAAAAGGAGAGACTTGTCTCAAGTGTGAGAGACTCAC 244
Qy 171 SerGlnLeuLeuGlySerTrpAspProTpgIuGluProGluAspAlaAlaProValAla 190
Db 245 TCCAGCTGCTGGGCTCTTGGAGCCGCTGGAGAAACCGAGAGACGAGCCCTGTGGCC 304
Qy 191 ProSerValProAlaSerGlyTyProGluLeuProThrProArgArgGluValGlnSer 210
Db 305 CCTCCGCTCCCTGCTCTGTGGTACCTTAGCTGCCCAACCCAGAGAGAGGTCCAGTCT 364
Qy 211 GluSerAlaGlnGlu----- 215
Db 365 GAAAGTCCCAAGACCAAGAGAGGAGTCCAGCCGAGCCAGAGGAGCGTGTGGTT 424
Qy 216 -----ProGlyAlaArgAspValGluAlaGlnLeuArgArgLeuGlnGluArg 232
Db 425 CTGAGCCCCCAGAGAGCAAGGATGTGAGGGCGAGCTGGCGGCTGTGAGAGAGAGAG 484
Qy 233 ThrGlyValValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeu 252
Db 485 AGGTCAAGGTGTGCTGAGACCGCGCGTGTCCATCGTCTTGTGCGGTGGCCACTG 544
Qy 253 ValCys-AlaGluCysAlaProGlyLeuGlnLeuCysProIleCys--ArgAlaProVa 271
Db 545 GTCTGTGCTGAGTGTGCCCCCGGCTGTGACGTGTGCCCATCTGGCAGAGAGCCCGTTC 604
Qy 271 ArgSerArg 274
Db 605 CCGCAGCCGG 614

RESULT 14

US-10-296-115-63
; Sequence 63, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 764PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 63
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-63

Alignment Scores:

Pred. No.: 2,31e-79 Length: 615
Score: 914.50 Matches: 173
Percent Similarity: 88.1% Conservative: 4
Best Local Similarity: 86.1% Mismatches: 4
Query Match: 53.1% Indels: 20
DB: 7 Gaps: 2

US-09-762-577b-12 (1-309) x US-10-296-115-63 (1-615)

Qy 94 PheTyAspTrpProLeuThrAlaGluValProProGluLeuLeuAlaAlaGlyPhe 113
Db 15 TGGTGAATTCGCGCTGACTGCTGAGTGGCCACCCGAGCTCTGCTGCTGCGCTTC 74
Qy 114 PheHisThrGlyHisGlnAspIlyValArgCysPhePheCysTyGlyGlyLeuGlnSer 133
Db 75 TTCACACAGCGCATAGAGCAAGGTGAGTGTCTTCTGTCTAAGGGGCGCTGACAGC 134
Qy 134 TrpIlyArgGlyAspAspProTrpThrGlyHisAlaIlySTrpPheProSerCysGlnPhe 153
Db 135 TGGAGCGCGGGAGCAAGCCCTGTGACGAGGAGTGCACAGTGTGTCCAGCTGTCAATTTC 194

Qy 154 LeuLeuArgSerIlyGlyArgAspPheValHisSerValGlnGluThrHisSerGlnLeu 173
Db 195 CTGCTCCGGTCAAAAGAGAGACTTGTCTCAAGTGTGACAGAGACTCACTCCAGCTG 254
Qy 174 LeuGlySerTrpAspProTpgIuGluProGluAspAlaAlaProValAlaProSerVal 193
Db 255 CTGGGCTCTTGGAGCCCGTGGAGAAACCGAGAGACGAGCCCTGTGGCCCTTCGCTC 314
Qy 194 ProAlaSerGlyTyProGluLeuProThrProArgArgGluValGlnSerIlySerIly 213
Db 315 CTGCTCTGTGGTACCTTAGCTGCCCAACCCAGAGAGAGGTCCAGTCTGAAAGTGC 374
Qy 214 GlnGlu----- 215
Db 375 CAGAGCCAGAGAGGAGTCACTCAGCCAGAGCCAGAGAGGAGCGTGTGGTTCTTGAGCC 434
Qy 216 ProGlyAlaArgAspValGluAlaGlnLeuArgArgLeuGlnGluArgThrCysIly 235
Db 435 CAGAGAGCAAGGATGTGAGGGCGAGCTGGCGGCTGTGAGAGAGAGAGAGAGAGAG 494
Qy 236 ValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeuValCys-Al 255
Db 495 GTGTGCTGTGACCGCGCGTGTCCATCGTCTTGTGCGGTGGCCACTGTGTGTGC 554
Qy 255 ArgIlyCysAlaProGlyLeuGlnLeuCysProIleCys--ArgAlaProValArgSerArg 274
Db 555 TGAAGTGTGCCCCCGGCTGTGACGTGTGCCCATCTGGCAGAGAGCCCGTCCGACGCG 614
Qy 274 g 274
Db 615 g 615

RESULT 15

US-10-723-860-8265
; Sequence 8265, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsaba
; APPLICANT: Ginsburg, Wendy M.
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8265
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-8265

Alignment Scores:

Pred. No.: 1,36e-74 Length: 858
Score: 867.00 Matches: 159
Percent Similarity: 99.4% Conservative: 0
Best Local Similarity: 99.4% Mismatches: 1
Query Match: 50.4% Indels: 0
DB: 8 Gaps: 0

US-09-762-577b-12 (1-309) x US-10-723-860-8265 (1-858)

Qy 150 SerCysGlnPheLeuLeuArgSerIlyGlyArgAspPheValHisSerValGlnGluThr 169
Db 193 AGCTGTCAAGTCTGCTCCGCTCAAAAGAGAGACTTGTCTCAAGTGTGACAGAGACT 252
Qy 170 HisSerGlnLeuLeuGlySerTrpAspProTpgIuGluProGluAspAlaAlaProVal 189
Db 253 CACTCCAGCTGTGGCTCTGTGGAGCCCGTGGAGAAACCGAGAGAGAGCCAGCCCTGTG 312

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QY 190 AlaProSerValProAlaSerGlyTyrProGluLeuProThrProArgArgGluValGln 209
Db 313 GCGCCCTCCGCTCGCTGCGGTACCTGAGCTGCCACACCAGGAGAGAGTCCAG 372
QY 210 SerGluSerAlaGlnGluProGlyAlaArgAspValGluAlaGlnLeuArgArgLeuGln 229
Db 373 TCTGAAGTGCCCGAGAGCCAGAGCCAGGATGTGGAGGCGCAGCTGCGGCGTGCAG 432
QY 230 GluGluArgThrCysIleValCysLeuAspArgAlaValSerIleValPheValProCys 249
Db 433 GAGGAGAGACGTCGACAGGTGTGCTGACCGCGCGTTCATCGTCTTGTGCCGTGC 492
QY 250 GlyHisLeuValCysAlaGluCysAlaProGlyLeuGlnLeuCysProIleCysArgAla 269
Db 493 GGCACCTGGTCTGTGTGAGTGTGCCCGGCTGCACTGTGCCCCCATCTGCAGAGCC 552
QY 270 ProValArgSerArgValArgThrPheLeuSer**AlaArgCysHisGlyArgProGly 289
Db 553 CCGCTCCGACGCGGTGCGCACCCTCTGCTAGGCCAGGTGCATGGCCGCGCAGGT 612
QY 290 GlyLeuGlnSerGlyLeuProAlaProLeuCysLeuPheThrValPheTrpAlaCys 309
Db 613 GGGCTGCAAGAGTGGGCTCCCTGCTGTGCTGTGACCTGTGTCTGGGCTTGC 672

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Search completed: April 19, 2006, 21:42:01
 Job time : 917 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 21:32:30 ; Search time 844 Seconds
(without alignments)
9839.108 Million cell updates/sec

Title: US-09-762-577B-11
Perfect score: 1246
Sequence: 1 cgcacacgagctcgtgcccg9.....agtgcgttcctccctgcgaagc 1246

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1228	98.6	1260	12	ADH89535
2	1228	98.6	1260	14	AEA36171
3	1228	98.6	1266	10	ACC72844
4	1228	98.6	1266	13	AD871346
5	1228	98.6	1376	4	AAF24856
6	1164	93.4	1322	10	ACC72843
7	1164	93.4	1322	13	AD871344
8	1162.4	93.3	1337	3	AAZ61210
9	1159.4	93.0	1363	3	AAAI5007
10	1159.4	93.0	1363	13	ADT88075
11	1021.4	82.0	1168	12	ADH89543
12	843	67.7	843	4	AAF24857
13	838	67.3	840	6	AAI42858
14	729.8	58.6	3782	5	AAAS91553
15	675	54.2	769	6	AAAI6365
16	650	52.2	723	6	AAI42856
17	649.4	52.1	672	6	AAI42857
18	640.6	51.4	858	12	ADQ25445
19	590	47.4	676	12	ADQ21628

20	535.2	43.0	1068	4	AAI16364	Adi16364 Human SBH
21	492.4	39.5	4810	12	ADH89542	Adh89542 Human Liv
22	449	36.0	449	12	ADQ21877	Adq21877 Human sof
23	434.2	34.8	615	4	AAH99228	Aah99228 Human pro
24	433.6	34.8	614	5	AAH91550	Aah91550 DNA encod
25	317.8	25.5	444	5	AAH91551	Aah91551 DNA encod
26	301.4	24.2	399	14	AEA39481	Aea39481 Human ML-
27	254	20.4	1531	10	ADFI7464	Adfi7464 Mouse IL-
28	224	18.0	226	11	ADJ13008	Adj13008 Human CDN
29	224	18.0	226	13	ADH83075	Adh83075 Human lym
30	204	16.4	204	6	AAI42854	AAI42854 Survivin-
31	200.2	16.1	539	13	ADQ51993	Adq51993 Novel can
32	160.4	12.9	404	5	AAF66690	AAF66690 Novel hum
33	141	11.3	141	6	AAI42855	AAI42855 Survivin-
34	135	10.8	200	10	ACA55618	ACA55618 Mouse sig
35	135	10.8	200	11	ADJ13051	Adj13051 Human CDN
36	135	10.8	200	12	ADJ15414	Adj15414 Human pol
37	135	10.8	200	13	ADH83128	Adh83128 Human lym
38	97	7.8	2474	6	ABK93873	ABK93873 Mouse inh
39	97	7.8	2673	8	ABZ58100	ABZ58100 Mouse inh
40	97	7.8	2676	2	AAV55042	AAV55042 Murine HI
41	93.8	7.5	2474	2	AAT70840	Aat70840 Mouse apo
42	91.8	7.4	3773	6	ABQ78228	Abq78228 Nucleotid
43	86.6	7.0	2862	2	AAT61592	Aat61592 Murine C-
44	86.6	7.0	3151	2	AAV55043	AAV55043 Murine HI
45	86.6	7.0	3151	8	ABZ58101	ABZ58101 Mouse inh

ALIGNMENTS

RESULT 1
ADH89535
ID ADH89535 standard; DNA; 1260 BP.
XX
AC ADH89535;
XX
DT 22-APR-2004 (first entry)
XX
DE Human Livin DNA.
XX
KW hyperproliferative disorder; aberrant apoptosis; human; ds; Livin; gene.
XX
OS Homo sapiens.
XX
PN US2004005565-A1.
XX
PD 08-JAN-2004.
XX
PE 02-JUL-2002; 2002US-00188646.
XX
PR 02-JUL-2002; 2002US-00188646.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KW;
XX
DR WPI; 2004-098436/10.
XX
DR P-PSDB; ADH89685.
XX
PT New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
XX
PS Example 13; SEQ ID NO 4; 60pp; English.
XX
CC The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding Livin and that specifically hybridizes with the nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The present sequence represents human Livin DNA.
XX

Sequence 1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;

Query Match 98.6%; Score 1228; DB 12; Length 1260;
Best Local Similarity 100.0%; Pred. No. 2,1e-260;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 19 GGCAGGCTGTGCTTATCCCTGCTGTCCTCCAGAGGTGGGCCCCGGGGGTCAAGAGACTCAG 78
Db 33 GGCAGGCTGTGCTTATCCCTGCTGTCCTCCAGAGGTGGGCCCCGGGGGTCAAGAGACTCAG 92
QY 79 AAGGCGCAGTGGGATATTCGAGATGAGCATCAGACCCCATTTCTGCTGCAACTG 138
Db 93 AAGGCGCAGTGGGATATTCGAGATGAGCATCAGACCCCATTTCTGCTGCAACTG 152
QY 139 GTCAGAGCCAGTGTTCCTCCATGAGACTTAAGACAGTGGCAGAGTCCCTGCAACCTGGA 198
Db 153 GTCAGAGCCAGTGTTCCTCCATGAGACTTAAGACAGTGGCAGAGTCCCTGCAACCTGGA 212
QY 199 CCACAGCCGAGACCTGTGGGAGCCGGGTGATGTGTCCACAGCAGAGCGCTGTGACCCGCG 258
Db 213 CCACAGCCGAGACCTGTGGGAGCCGGGTGATGTGTCCACAGCAGAGCGCTGTGACCCGCG 272
QY 259 TCTCTGGGAGACCTGTCTCTAGAGCTGAGACCTGAGAGCCTGGGAGCAACGTGATGGG 318
Db 273 TCTCTGGGAGACCTGTCTCTAGAGCTGAGACCTGAGAGCCTGGGAGCAACGTGATGGG 332
QY 319 CAGATCTCTGGGAGCAGCTGGGAGCCCTCTGACAGAGAGAGAGAGAGAGGCGCGGGGCGC 378
Db 333 CAGATCTCTGGGAGCAGCTGGGAGCCCTCTGACAGAGAGAGAGAGAGAGGCGCGGGGCGC 392
QY 379 ACCTGTGTCAGAGGGGCGCTGCTCCCGGAGATGGGCTCTGAGAGATTTGGTCTGGCTTCG 438
Db 393 ACCTGTGTCAGAGGGGCGCTGCTCCCGGAGATGGGCTCTGAGAGATTTGGTCTGGCTTCG 452
QY 439 TTCTATATCTGGCCGCTGACTGCTGAGGTGCAACCCAGCTGTGCTGCTGCTCCGAGCTTC 498
Db 453 TTCTATATCTGGCCGCTGACTGCTGAGGTGCAACCCAGCTGTGCTGCTGCTCCGAGCTTC 512
QY 499 TTCCACACAGGCGCATCAGGACAGAGTGAAGTCTTTCTTCTGCTATGAGGAGGCTCTGAGAGC 558
Db 513 TTCCACACAGGCGCATCAGGACAGAGTGAAGTCTTTCTTCTGCTATGAGGAGGCTCTGAGAGC 572
QY 559 TGAAGGCGCGGAGACGACCCCTGAGACGAGCATGCCAAGTGGTTCCTCCAGCTGTCAAGTTC 618
Db 573 TGAAGGCGCGGAGACGACCCCTGAGACGAGCATGCCAAGTGGTTCCTCCAGCTGTCAAGTTC 632
QY 619 CTGCTCCGCTCAAAAGAGAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTG 678
Db 633 CTGCTCCGCTCAAAAGAGAGACTTTGTTCACAGTGTGACAGAGACTCACTCCAGCTG 692
QY 679 CTGGGCTCTGGGAGCCGCTGGAGAAACGAGAACGCGCCCTGTGGCCCTCCCTCCCTC 738
Db 693 CTGGGCTCTGGGAGCCGCTGGAGAAACGAGAACGCGCCCTGTGGCCCTCCCTCCCTC 752
QY 739 CTGCTCTTGGGATACCTTGAGTGTCCACACCCAGAGAGAGAGTCCAGTCTGAAGTCC 798
Db 753 CTGCTCTTGGGATACCTTGAGTGTCCACACCCAGAGAGAGAGTCCAGTCTGAAGTCC 812
QY 799 CAGGAGCCAGAGAGCAGAGGATGTGAGAGGGGAGCTGCGCGGCTCTCAGAGAGAGAGAGC 858
Db 813 CAGGAGCCAGAGAGCAGAGGATGTGAGAGGGGAGCTGCGCGGCTCTCAGAGAGAGAGAGC 872
QY 859 TGCAGAGTGTGCTGAGACCGCGCTGTTCATGCTCTTGTGTCGCTGTGGGCACTGGTTC 918
Db 873 TGCAGAGTGTGCTGAGACCGCGCTGTTCATGCTCTTGTGTCGCTGTGGGCACTGGTTC 932
QY 919 TGTGCTGAGTGTGCCCCCGGAGCTGACGTGTGCTCCCATCTGTGAGAGCCCGCTCGCAGC 978
Db 933 TGTGCTGAGTGTGCCCCCGGAGCTGACGTGTGCTCCCATCTGTGAGAGCCCGCTCGCAGC 992
QY 979 CGCGTGCAGACCTTCTGTCTTCTAGGCGCAGAGTGCATGCGCGGCGCAGAGTGGGCTCAGAGT 1038
Db 993 CGCGTGCAGACCTTCTGTCTTCTAGGCGCAGAGTGCATGCGCGGCGCAGAGTGGGCTCAGAGT 1052

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QY 1039 GGGCTCCCTGCCCCCTCTCTGCTGCTGTTCTGAGCTGATGTTGTGGGCGCTGTGAGATGGCAG 1098
Db 1053 GGGCTCCCTGCCCCCTCTCTGCTGCTGTTCTGAGCTGATGTTGTGGGCGCTGTGAGATGGCAG 1112
QY 1099 AGCTGATGTCATTCAGACACTGACAGCCCTGATTTCCCGAGCACCCCGCAGAGGTGAGAG 1158
Db 1113 AGCTGATGTCATTCAGACACTGACAGCCCTGATTTCCCGAGCACCCCGCAGAGGTGAGAG 1172
QY 1159 AGGAGGCCCTTCTGGCGGTGGGAGATGAGCTTAACCTGATACCTGTTGATGCTTGAT 1218
Db 1173 AGGAGGCCCTTCTGGCGGTGGGAGATGAGCTTAACCTGATACCTGTTGATGCTTGAT 1232
QY 1219 AGAATAAAGTGGGTTTTCCTCGAGAGT 1246
Db 1233 AGAATAAAGTGGGTTTTCCTCGAGAGT 1260

```

RESULT 2
AEA36171
ID AEA36171 standard; DNA, 1260 BP.
XX
AC AEA36171;
XX
DT 25-AUG-2005 (first entry)
XX
DE Human nucleic acid sequence #103.
XX
KW Screening; gene expression; colorectal tumor; colitis; Crohns disease;
KW Irritable bowel syndrome; gastrointestinal disease; cytostatic;
KW Gastrointestinal-gen.; antiinflammatory; de.
XX
OS Homo sapiens.
XX
PN WO2005054507-A2.
XX
PD 16-JUN-2005.
XX
PF 03-DEC-2004; 2004WO-GB005078.
XX
PR 04-DEC-2003; 2003GB-00028048.
XX
PA (UTSH-) UNIV SHEFFIELD.
XX
PI Corfe B, Chirakkal H;
XX
DR MPI; 2005-435407/44.
XX
PT Screening for nucleic acid molecules exhibiting altered expression in
PT cells grown in the presence of butyrate, and detection of the nucleic
PT acid molecules or the encoded polypeptides in diagnosing colorectal
PT cancer.
XX
PS Disclosure; Page 143; 266pp; English.
XX
CC The invention relates to a method of screening for nucleic acid molecules
CC that show altered expression in a first cell sample comprising comparing
CC the gene expression profile of the sample with that of a second reference
CC sample, where the first sample has been grown in the presence of butyrate
CC or a related carbon source from which butyrate is directly or indirectly
CC derived, but the reference sample has not. The invention also relates to
CC a method of detecting at least one nucleic acid molecule associated with
CC the initiation and/or progression of colorectal cancer in an animal,
CC comprising providing a biological sample comprising at least one cell to
CC be tested, contacting the sample with a ligand (preferably a hybridizing
CC nucleic acid molecule) which binds to at least one nucleic acid and
CC detecting the presence of at least one molecule in the sample, a method
CC of detecting at least one polypeptide associated with the initiation
CC and/or progression of colorectal cancer in an animal comprising providing
CC a biological sample comprising at least one cell to be tested, contacting
CC the sample with at least one ligand that specifically binds at least one
CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising
CC an amino acid sequence which varies by the addition, deletion or

PI Afar D, Aziz N, Gish KC, Heyezi PA, Mack DH, Wilson KE;
 PI Zlotnik A;
 DR WPI; 2003-354600/3.
 DR P-PDB; ABR58693.
 XX
 PT New genes that are up-regulated or down-regulated in cancers, useful as
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 PT therapeutic targets for screening drugs for treating these diseases.
 PS
 PS Claim 8; Page 725-726; 767pp; English.

The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
 CC related gene nucleotide sequences which encode the proteins given in
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies

Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;

Query Match 98.6%; Score 1228; DB 10; Length 1268;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-260;
 Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 19 GGCAGGCGCTGCTATCCCTGCTGTCCTCCAGGAGTGGGCGCCGGGGGTGAGAGCTCGAG 78
Db 33 GGCAGGCGCTGCTATCCCTGCTGTCCTCCAGGAGTGGGCGCCGGGGGTGAGAGCTCGAG 92
QY 79 AAGGGCCAGCTGGGACATATCTGAGATTGGCCATCAAGCCCATTTCTGCTCAAACTGG 138
Db 93 AAGGGCCAGCTGGGACATATCTGAGATTGGCCATCAAGCCCATTTCTGCTCAAACTGG 152
QY 139 GTCAAGGCCAGTGTTCCTTCATGGAGCCTTAAAGACAGTGCACAGCTGCAACCTGGA 198
Db 153 GTCAAGGCCAGTGTTCCTTCATGGAGCCTTAAAGACAGTGCACAGCTGCAACCTGGA 212
QY 199 CCACAGCCGAGCCTAGGGGAGCGGGTGAATGCTCCACGACAGAGCGCTGAGACCCGCG 258
Db 213 CCACAGCCGAGCCTAGGGGAGCGGGTGAATGCTCCACGACAGAGCGCTGAGACCCGCG 272
QY 259 TCTCTGGGAGCGCTGTCTTAGGCTTGACACCTGCAAGCTGAGGACCACTGGAATGG 318
Db 273 TCTCTGGGAGCGCTGTCTTAGGCTTGACACCTGCAAGCTGAGGACCACTGGAATGG 332
QY 319 CAGATCTGGGAGCGCTGCGGCGCTGACAGAGAGGAAAGAGAGAGGCGCGGAGCC 378
Db 333 CAGATCTGGGAGCGCTGCGGCGCTGACAGAGAGGAAAGAGAGAGGCGCGGAGCC 392
QY 379 ACCCTGTCCAGGAGGCGCTGCTTCCCGGACATGGGCTCTGAGAGATTGCGTGGCTCC 438
Db 393 ACCCTGTCCAGGAGGCGCTGCTTCCCGGACATGGGCTCTGAGAGATTGCGTGGCTCC 452
QY 439 TTCTATGACTGGCGCTGACTGCTGAGGTGCACCCGAGCTGCGCTGCTGCGGCTTC 498
Db 453 TTCTATGACTGGCGCTGACTGCTGAGGTGCACCCGAGCTGCGCTGCTGCGGCTTC 512
QY 499 TTCACACAGGCGCATCAGAGACAGGTGAGGTCTTTCTTCTGCTATGAGGGCGCTGCAAGC 558

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Db 513 TTCACACAGGCGCATCAGAGACAGGTGAGGTCTTTCTTCTGCTATGAGGGCGCTGCAAGC 572
QY 559 TGAAGCGCGGGAGACACCCCTTGAGACGACATGCCAAGTGTTCCTCCAGCTGTCAATTTC 618
Db 573 TGAAGCGCGGGAGACACCCCTTGAGACGACATGCCAAGTGTTCCTCCAGCTGTCAATTTC 632
QY 619 CTGCTCCGGTCAAAAGAGAGACTTTGTTCACAGTGTGACAGAGACTCACTCCAGCTG 678
Db 633 CTGCTCCGGTCAAAAGAGAGACTTTGTTCACAGTGTGACAGAGACTCACTCCAGCTG 692
QY 679 CTGGGCTCTTGGAGACCCCTTGAGAGAACCGAGAACCGAGCCCTGTGAGCCCTCCGTC 738
Db 693 CTGGGCTCTTGGAGACCCCTTGAGAGAACCGAGAACCGAGCCCTGTGAGCCCTCCGTC 752
QY 739 CTTGCTCTGGGTACCTTGAGCTGCGCACACCCAGAGAGAGTCACTGAGAAAGTCC 798
Db 753 CTTGCTCTGGGTACCTTGAGCTGCGCACACCCAGAGAGAGTCACTGAGAAAGTCC 812
QY 799 CAGAGCCAGAGACCAAGGATGTGAGAGCGGAGCTGCGGCGCTGACAGAGAGAGAGC 858
Db 813 CAGAGCCAGAGACCAAGGATGTGAGAGCGGAGCTGCGGCGCTGACAGAGAGAGAGC 872
QY 859 TGCAAGTGTGCTGAGACCGGCGGTGTCATGTCCTTTGTGCTGCGGACACTGCTC 918
Db 873 TGCAAGTGTGCTGAGACCGGCGGTGTCATGTCCTTTGTGCTGCGGACACTGCTC 932
QY 919 TGTGCTGAGTGTGCCCCGCTGCAAGCTGTGCCCATTTGTCAGAGAGCCCGTCCGAGC 978
Db 933 TGTGCTGAGTGTGCCCCGCTGCAAGCTGTGCCCATTTGTCAGAGAGCCCGTCCGAGC 992
QY 979 GCGGTGCGACACTTCTGCTCTAGGCCAGATGTCATGCGCGGACAGTGGTGGCTGACAGT 1038
Db 993 GCGGTGCGACACTTCTGCTCTAGGCCAGATGTCATGCGCGGACAGTGGTGGCTGACAGT 1052
QY 1039 GAGCTCCCTGCGCTCTCTGCTGCTGTGTGAGACTGTGTTGGGCGCTGAGAGATGGCAG 1098
Db 1053 GAGCTCCCTGCGCTCTCTGCTGCTGTGTGAGACTGTGTTGGGCGCTGAGAGATGGCAG 1112
QY 1099 AGCTGTGTGCATCAGACACTGACAGAGCCCTGATTTCCCGACACCGCCAGGAGTGAAG 1158
Db 1113 AGCTGTGTGCATCAGACACTGACAGAGCCCTGATTTCCCGACACCGCCAGGAGTGAAG 1172
QY 1159 AGAGGCGCTTGTGCTGAGCGTGGGAGATGCTTAAGCTGTGTTGATGCTTGAAT 1218
Db 1173 AGAGGCGCTTGTGCTGAGCGTGGGAGATGCTTAAGCTGTGTTGATGCTTGAAT 1232
QY 1219 AGAAATTAAGTGGTTCCTCTGAGGT 1246
Db 1233 AGAAATTAAGTGGTTCCTCTGAGGT 1260

```

RESULT 4
 ADS71346
 ID ADS71346 standard; DNA; 1268 BP.
 XX
 AC ADS71346;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human livin beta splice variant DNA.
 XX
 KW Immune response; cancer-associated inhibitor of Apoptosis-family protein;
 KW IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma;
 KW human; livin beta; gene; ds; immunostimulant; cytostatic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 174..1016
 FT /tag= a
 FT /product= "Human livin beta splice variant protein"
 PN US2004192631-A1.

XX 30-SEP-2004.
 PD 24-MAR-2004; 2004US-00807897.
 XX 24-MAR-2003; 2003US-0457009P.
 PR
 XX (XIAN/) XIANG R.
 XX (ZHOU/) ZHOU H.
 PA (REIS/) REISFELD R. A.
 XX
 PI Xiang R, Zhou H, Reisfeld RA,
 XX
 DR WPI; 2004-689881/67.
 DR P-PSDB; ADS71347.
 DR RERSSEQ; NM_022161.

XX New DNA vaccine comprising a cancer-associated inhibitor of Apoptosis-
 PT family protein immunoreactive gene product, useful for eliciting an immune
 response against cancer.

XX Claim 26; SEQ ID NO 28; 84bp; English.

XX The present invention relates to a DNA vaccine effective for eliciting an
 CC immune response against cancer cells which comprises a DNA construct
 CC operably encoding at least one cancer-associated inhibitor of Apoptosis-
 CC family protein (IAP-family protein) and at least one immunoreactive gene
 CC product in a pharmaceutical carrier. The invention is useful for treating
 CC cancer such as lung cancer, colorectal cancer and melanoma. The present
 CC sequence is the human livin beta splice variant DNA.

XX Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;

Query Match 98.6%; Score 1228; DB 13; Length 1268;
 Best Local Similarity 100.0%; Pred. No. 2,1e-260;
 Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGCAGGCGCTGCTATCCCTGCTGTCCTCCAGGGTGGGCGCGGGGCTCAGAGCTCCAG 78
 Db 33 GGCAGGCGCTGCTATCCCTGCTGTCCTCCAGGGTGGGCGCGGGGCTCAGAGCTCCAG 92
 QY 79 AAGGCGCAGCTGGGCAATTTCTGAGATTGGCCATCAAGCCCATTTCTGCTGCAAACTG 138
 Db 93 AAGGCGCAGCTGGGCAATTTCTGAGATTGGCCATCAAGCCCATTTCTGCTGCAAACTG 152
 QY 139 GTCAGAGCGAGTGTTCCTCCATGAGGACTTAAAGACAGTGCAGTGCCTGCAACCTG 198
 Db 153 GTCAGAGCGAGTGTTCCTCCATGAGGACTTAAAGACAGTGCAGTGCCTGCAACCTG 212
 QY 199 CCACAGCGGAGCCACTGGGAGCGGGTGTGCTCCACGAGGAGCGCTGAGACCCCGC 258
 Db 213 CCACAGCGGAGCCACTGGGAGCGGGTGTGCTCCACGAGGAGCGCTGAGACCCCGC 272
 QY 259 TCTCTGGGAGCCCTGCTCTAAGGCTTGAGACCTGCAAGGCTTGAGACCACTGATGAG 318
 Db 273 TCTCTGGGAGCCCTGCTCTAAGGCTTGAGACCTGCAAGGCTTGAGACCACTGATGAG 332
 QY 319 CAGATCTGGGCGCAGCTGCGGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
 Db 333 CAGATCTGGGCGCAGCTGCGGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
 QY 379 ACCCTGTCAGAGGGGCGCTGCTCCCGGAGTGGGCTCTGAGAGATTGGCGCTGAGCCCTCC 438
 Db 393 ACCCTGTCAGAGGGGCGCTGCTCCCGGAGTGGGCTCTGAGAGATTGGCGCTGAGCCCTCC 452
 QY 439 TTCTATGACTGGCGCTGACTGCTGAGGTGCAACCGGAGCTGAGCTGCTGCGGAGCTTC 498
 Db 453 TTCTATGACTGGCGCTGACTGCTGAGGTGCAACCGGAGCTGAGCTGCTGCGGAGCTTC 512
 QY 499 TTCCACACAGGCGCATCAGAGCAAGGTAGAGTCTTTCTGCTATGAGGGGCGCTGCAAGC 558
 Db 513 TTCCACACAGGCGCATCAGAGCAAGGTAGAGTCTTTCTGCTATGAGGGGCGCTGCAAGC 572

QY 559 TGAAGCGCGGGAGCAGACCCCTGAGCAGAGCATGCCAAGTGTCTCCACAGCTGCACTTC 618
 Db 573 TGAAGCGCGGGAGCAGACCCCTGAGCAGAGCATGCCAAGTGTCTCCACAGCTGCACTTC 632
 QY 619 CTGCTCCGGTCAAAAGAGAGACTTGTTCACAGTGTGAGAGAGACTCACTCCCACTG 678
 Db 633 CTGCTCCGGTCAAAAGAGAGACTTGTTCACAGTGTGAGAGAGACTCACTCCCACTG 692
 QY 679 CTGGGCTCTGGGAGCCCGTGGGAGAGACCGGAGAGACCGGAGAGAGAGAGAGAGAGAG 738
 Db 693 CTGGGCTCTGGGAGCCCGTGGGAGAGACCGGAGAGACCGGAGAGAGAGAGAGAGAGAG 752
 QY 739 CTTGCTCTGGGAGTCCCTGAGCTGCGCAGACCCAGAGAGAGTCCAGTCTGAAGTGC 798
 Db 753 CTTGCTCTGGGAGTCCCTGAGCTGCGCAGACCCAGAGAGAGTCCAGTCTGAAGTGC 812
 QY 799 CAGAGCCAGAGCCAGAGATGTGAGAGCCGAGCTGCGGCGCTGAGAGAGAGAGAGAG 858
 Db 813 CAGAGCCAGAGCCAGAGATGTGAGAGCCGAGCTGCGGCGCTGAGAGAGAGAGAGAG 872
 QY 859 TGCAGAGTGTGCTGAGACCGGCGCTGCTGATGCTTTGTCCTGTCGCGGCACTGCTC 918
 Db 873 TGCAGAGTGTGCTGAGACCGGCGCTGCTGATGCTTTGTCCTGTCGCGGCACTGCTC 932
 QY 919 TGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 978
 Db 933 TGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 992
 QY 979 CGGCTGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
 Db 993 CGGCTGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
 QY 1039 GGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098
 Db 1053 GGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1112
 QY 1099 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1158
 Db 1113 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
 QY 1159 AGAGAGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1218
 Db 1173 AGAGAGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
 QY 1219 AGAAATTAAGTGGGTTTCCCTGAGGT 1246
 Db 1233 AGAAATTAAGTGGGTTTCCCTGAGGT 1260

RESULT 5
 AAF24856
 ID AAF24856 standard; cDNA; 1376 BP.
 AC AAF24856;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of an apoptosis inhibitor designated livin.
 XX
 KW Livin; apoptosis inhibitor; IAP-3; cancer; apoptosis; gene therapy;
 KM melanoma; Alzheimer's disease; Parkinson's disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 211..1053
 FT /*tag= a
 FT /product= "livin"
 XX
 PN W0200077201-A1.
 XX
 PD 21-DEC-2000.

PF 09-JUN-2000; 2000MO-GB002272.
XX
XX 15-JUN-1999; 99US-0139291P.
XX
XX (ASTR) ASTRAZENCA AB.
PA (ASTR) ASTRAZENCA UK LTD.
XX
XX
PI Gomes BC, Kasof GM, Prosser JC;
XX WPI: 2001-122843/13.
DR P-PSDB; AAB31478.
XX
XX Novel livin polypeptides and polynucleotides useful for treating
PT pathophysiological disorders related to apoptosis, cancers, particularly
PT melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gene
PT therapy.
XX
XX Claim 8; Page 53-54; 62pp; English.
XX
XX The present sequence encodes a human polypeptide, designated livin. Livin
CC is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in
CC certain cancer cell lines and prevents apoptosis. The livin polypeptide
CC is useful for identifying compounds that inhibit and modulate livin
CC function and activity. Such compounds are useful in the treatment of a
CC dysfunctional apoptosis condition. Livin polypeptides are useful as a
CC source of probes and primers, and in gene therapy. Livin polypeptides and
CC polynucleotides, their inhibitors and modulators are useful for treating
CC pathophysiological disorders related to apoptosis, cancers, particularly
CC melanoma cancer, Alzheimer's disease and Parkinson's disease
XX
XX Sequence 1376 BP; 233 A; 432 C; 454 G; 257 T; 0 U; 0 Other;
SO
Query Match 98.6%; Score 1228; DB 4; Length 1376;
Best Local Similarity 100.0%; Pred. No. 2.1e-260;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 GGCAGGCTGTGCTATCCCTGCTGTCCTCCAGAGGTGGGCGCGGGGTGAGAGCTCCAG 78
DB 70 GGCAGGCTGTGCTATCCCTGCTGTCCTCCAGAGGTGGGCGCGGGGTGAGAGCTCCAG 129
QY 79 AAGGGCCAGCTGGGCAATATCTGAGATTGGCATGACCCCATTTCTGTGCAACCTG 138
DB 130 AAGGGCCAGCTGGGCAATATCTGAGATTGGCATGACCCCATTTCTGTGCAACCTG 189
QY 139 GTGAGGCCAGTGTTCCTCTCATGGGACCTTAAAGACAGTGCACCTGACCCGTGA 198
DB 190 GTGAGGCCAGTGTTCCTCTCATGGGACCTTAAAGACAGTGCACCTGACCCGTGA 249
QY 199 CCAAGCCGAGCCTGAGGAGCGGATGATGTCACCAAGAGAGGCTGTGACCCCGC 258
DB 250 CCAAGCCGAGCCTGAGGAGCGGATGATGTCACCAAGAGAGGCTGTGACCCCGC 309
QY 259 TCTTGGGAGAGCCCTGTCTTAAAGCTGACACCTGTGAGACCTGAGCCAGTGA 318
DB 310 TCTTGGGAGAGCCCTGTCTTAAAGCTGACACCTGTGAGACCTGAGCCAGTGA 369
QY 319 CAGATCCTGGGAGAGTGGGCGCCCTGACAGAGAGAGAGAGAGAGAGGCGCGG 378
DB 370 CAGATCCTGGGAGAGTGGGCGCCCTGACAGAGAGAGAGAGAGAGAGGCGCGG 429
QY 379 ACCCTGTCCAGAGGCGCTCTCCCGGACATGGGCTGAGAGAGTGGGCTGAGC 438
DB 430 ACCCTGTCCAGAGGCGCTCTCCCGGACATGGGCTGAGAGAGTGGGCTGAGC 489
QY 439 TTTCTATGATGCGCGCTGACTGCTGAGTGCACCCGAGCTGTGCTGCGGCTTC 498
DB 490 TTTCTATGATGCGCGCTGACTGCTGAGTGCACCCGAGCTGTGCTGCGGCTTC 549
QY 499 TTCACACAGGCGCATCAGGACAAAGTGAAGTGTCTTCTGTATGGGGGCTGAGAGC 558
DB 550 TTCACACAGGCGCATCAGGACAAAGTGAAGTGTCTTCTGTATGGGGGCTGAGAGC 609
QY 559 TGGAAAGCGGGAGAGAGCCCTGAGAGGAGCATGCAAGTGGTTCCTCAGCTGTCA 618

DB 610 TGGAAAGCGGGAGAGAGCCCTGAGAGGAGATGCCAATGTGTCCCGAGCTGTCA 669
QY 619 CTGCTCCGGTCAAAAGAGAGACTTGTTCACAGAGTGTGAGAGAGACTCACTCCAGCTG 678
DB 670 CTGCTCCGGTCAAAAGAGAGACTTGTTCACAGAGTGTGAGAGAGACTCACTCCAGCTG 729
QY 679 CTGAGGCTCTGGAGACCCGTGGAGAGAACCGGAAGAGAGAGCCCTGTGGCCCTCCGTC 738
DB 730 CTGAGGCTCTGGAGACCCGTGGAGAGAACCGGAAGAGAGAGCCCTGTGGCCCTCCGTC 789
QY 739 CTTGCTCTGGAGACCCGTGGAGAGAACCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 798
DB 790 CTTGCTCTGGAGACCCGTGGAGAGAACCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 849
QY 799 CAGAGCCAG 858
DB 850 CAGAGCCAG 909
QY 859 TGCAGAGTGTGCTGAGACCGGCGCTGTTCATGCTTGTGCGGTGCGGCACTGTGTC 918
DB 910 TGCAGAGTGTGCTGAGACCGGCGCTGTTCATGCTTGTGCGGTGCGGCACTGTGTC 969
QY 919 TGTGCTGAGTGTGCCCCGAGCTGTGAGCTGTGCCCCATCTGCAAGAGCCCGTCCGAGC 978
DB 970 TGTGCTGAGTGTGCCCCGAGCTGTGAGCTGTGCCCCATCTGCAAGAGCCCGTCCGAGC 1029
QY 979 CCGGTGCGGCACTTCTCTCTAGGCGAGGTGCCATGCGGCGGAGAGTGGGCTGAGAGT 1038
DB 1030 CCGGTGCGGCACTTCTCTCTAGGCGAGGTGCCATGCGGCGGAGAGTGGGCTGAGAGT 1089
QY 1039 GGGCTCCGAGCCCTCTGCTGTGCTGTGAGCTGTGAGGCTGTGAGATGGAG 1098
DB 1090 GGGCTCCGAGCCCTCTGCTGTGCTGTGAGCTGTGAGGCTGTGAGATGGAG 1149
QY 1099 AGCTGTGCTCATCAGACCTGATGATTCGCCAGCACCGCCAGAGGTGAGAG 1158
DB 1150 AGCTGTGCTCATCAGACCTGATGATTCGCCAGCACCGCCAGAGGTGAGAG 1209
QY 1159 AGGAGCCCTGCTTGGGAGTGGGAGTGGCTTAACTGATCTGTGGATGCTTGAAT 1218
DB 1210 AGGAGCCCTGCTTGGGAGTGGGAGTGGCTTAACTGATCTGTGGATGCTTGAAT 1269
QY 1219 AGAATTAAGTGGTTCCTGAGAGT 1246
DB 1270 AGAATTAAGTGGTTCCTGAGAGT 1297
RESULT 6
ID ACC72843 standard; cDNA; 1322 BP.
XX
XX ACC72843;
AC
XX
DT 09-JUN-2003 (first entry)
XX
XX Human cancer related protein encoding cDNA SEQ ID NO:181.
DE
XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometrial; gene; ss.
OS Homo sapiens.
XX
XX MO2003025138-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 17-SEP-2002; 2002MO-US029560.
XX
XX PR 17-SEP-2001; 2001US-0323469P.
XX
XX PR 20-SEP-2001; 2001US-0323887P.
XX
XX PR 13-NOV-2001; 2001US-0350666P.
XX
XX PR 08-FEB-2002; 2002US-0355145P.

PR 08-FEB-2002; 2002US-0355257P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Afar D, Aziz N, Gish KC, Heveri PA, Mack DH, Wilson KE;
 PI Zlotnick A;
 XX WPI; 2003-354600/33.
 DR P-PSDB; ABR58692.
 XX
 PT New genes that are up-regulated or down-regulated in cancers, useful as
 PT makers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 PT therapeutic targets for screening drugs for treating these diseases.
 XX
 PS Claim 8; Page 725; 767pp; English.
 XX
 CC The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
 CC related gene nucleotide sequences which encode the proteins given in
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies
 CC
 SQ Sequence 1322 BP; 212 A; 417 C; 445 G; 248 T; 0 U; 0 Other;
 Query Match 93.4%; Score 1164; DB 10; Length 1322;
 Best Local Similarity 95.8%; Pred. No. 2.5e-246;
 Matches 1228; Conservative 0; Mismatches 0; Indels 54; Gaps 1;

QY 19 GGCAGGCGCTGCTGCTATCCCTGCTGCTGCCAGGGTGGGCCCCGGGGGTCAGAGACTCCAG 78
 DB |||||
 DB 33 GGCAGGCGCTGCTGCTATCCCTGCTGCTGCCAGGGTGGGCCCCGGGGTTCAGAGACTCCAG 92
 QY 79 AAGGGCCAGCTGGGCATATTTCTGAGATTGGCCATCAGCCCCCATTTTCTGCTGCAAACTTG 138
 DB |||||
 DB 93 AAGGGCCAGCTGGGCATATTTCTGAGATTGGGCATCAGCCCCCATTTTCTGCTGCAAACTTG 152
 QY 139 GTCAAGCCAGTGTTCCTCCATGGAAGCTTAAGAGACAGTGCAGAGCTGTCACCGTGA 198
 DB |||||
 DB 153 GTCAAGCCAGTGTTCCTCCATGGAAGCTTAAGAGACAGTGCAGAGCTGTCACCGTGA 212
 QY 199 CCAAGCCGAGGCACTGGGAGCCGGGATGTCGCCAGAGAGCCCTGTGAGACCCCGC 258
 DB |||||
 DB 213 CCAAGCCGAGGCACTGGGAGCCGGGATGTCGCCAGAGAGCCCTGTGAGACCCCGC 272
 QY 259 TCTCTGGGCAAGCCCTGTCTAGGCTTGAACCTGAGAGCTTGGAGCAAGTGTGATGG 318
 DB |||||
 DB 273 TCTCTGGGCAAGCCCTGTCTAGGCTTGAACCTGAGAGCTTGGAGCAAGTGTGATGG 332
 QY 319 CAGATCTCTGGGCAAGCTTGGGCCCCCTGACAGAGAGAGAGAGAGAGGCGCCCGGGCC 378
 DB |||||
 DB 333 CAGATCTCTGGGCAAGCTTGGGCCCCCTGACAGAGAGAGAGAGAGAGGCGCGCGGGCC 392
 QY 379 ACCCTGTCAGAGGGGCGCTGCTTCCCGGAGATGGGCTCTAGAGAGTGGTGTGAGCTCC 438
 DB |||||
 DB 393 ACCCTGTCAGAGGGGCGCTGCTTCCCGGAGATGGGCTCTAGAGAGTGGTGTGAGCTCC 452
 QY 439 TTCTATGACTGGCGCTGACTGCTGAGGTGCACCCGAGCTGTGCTGCGCGCTTC 498

DB 453 TTCTATGACTGGCGCTGACTGACTGAGGTGCACCCGAGCTGTGGCTGTGCTCGCGGCTTC 512
 QY |||||
 QY 499 TTCCACACAGGCCCATTCACAGCAAGGTGAGTGTCTTCTTCTGCTATTTGGGGGCTTCACAGC 558
 DB |||||
 DB 513 TTCCACACAGGCCCATTCACAGCAAGGTGAGTGTCTTCTTCTGCTATTTGGGGGCTTCACAGC 572
 QY 559 TGAAGGCGGGGAGCAGCCCTGTGAGCAGAGCATGCCAAGTGTGTTCCCGAGCTGCAGTTC 618
 DB |||||
 DB 573 TGAAGGCGGGGAGCAGCCCTGTGAGCAGAGCATGCCAAGTGTGTTCCCGAGCTGCAGTTC 632
 QY 619 CTGCTCGGTCAAAAGAGAGACTTGTGTCACAGTGTGACAGAGACTCACTCCAGCTG 678
 DB |||||
 DB 633 CTGCTCGGTCAAAAGAGAGACTTGTGTCACAGTGTGACAGAGACTCACTCCAGCTG 692
 QY 679 CTGGGCTCTGGGAGCAGCCCTGTGAGGAGAACCCGAGAGACCCAGCTGTGCGCCCTCCGTC 738
 DB |||||
 DB 693 CTGGGCTCTGGGAGCAGCCCTGTGAGGAGAACCCGAGAGACCCAGCTGTGCGCCCTCCGTC 752
 QY 739 CTGCGCTTGGGATACCTGAGCTGCGCCACACCGAGAGAGAGTCCAGTCCGAAAGTGC 798
 DB |||||
 DB 753 CTGCGCTTGGGATACCTGAGCTGCGCCACACCGAGAGAGAGTCCAGTCCGAAAGTGC 812
 QY 799 CAGAG----- 804
 DB 813 CAGAGCCAGAGAGGGGTCACTCCAGCCGAGGCCCCAGAGGGCGTGTGGTCTTGAAGCC 872
 QY 805 CCAAGAGCCAGAGATGTGAGGCGCAGCTGCGCGCTGACAGAGAGAGAGAGAGTGCAG 864
 DB |||||
 DB 873 CCAAGAGCCAGAGATGTGAGGCGCAGCTGCGCGCTGACAGAGAGAGAGAGAGTGCAG 932
 QY 865 GTGTGCTGAGACCGGCGGTGTCATGCTGTTGTGTCGGGCGGACCTGTGCTGTGCT 924
 DB |||||
 DB 933 GTGTGCTGAGACCGGCGGTGTCATGCTGTTGTGTCGGGCGGACCTGTGCTGTGCT 992
 QY 925 GAGTGTGCCCCCGGCTGACAGTGTGCCCATCTGAGAGAGCCCGCTGCGACCGCGTG 984
 DB |||||
 DB 993 GAGTGTGCCCCCGGCTGACAGTGTGCCCATCTGAGAGAGCCCGCTGCGACCGCGTG 1052
 QY 985 CGACACTTCTGTCTGATGAGCAGAGTGCATGCGCGGCGAGGTGGCTGACAGTGGGCTC 1044
 DB |||||
 DB 1053 CGACACTTCTGTCTGATGAGCAGAGTGCATGCGCGGCGAGGTGGCTGACAGTGGGCTC 1112
 QY 1045 CCTGCCCTCTGCGCTTCTGAGCTGTGTCGAGTGTGAGGCGCTGAGAGATGGCAGAGCTGG 1104
 DB |||||
 DB 1113 CCTGCCCTCTGCGCTTCTGAGCTGTGTCGAGTGTGAGGCGCTGAGAGATGGCAGAGCTGG 1172
 QY 1105 TGTCAATCAGACATGACAGCAGCCCTGATTCCCGACACACCGCCAGAGGTGAGAGAGG 1164
 DB |||||
 DB 1173 TGTCAATCAGACATGACAGCAGCCCTGATTCCCGACACACCGCCAGAGGTGAGAGAGG 1232
 QY 1165 CCTTCTCTGGCGTGGGGAGATGCTTAACCTGATCCTGTTGATGCTTCTGAATAGAAAT 1224
 DB |||||
 DB 1233 CCTTCTCTGGCGTGGGGAGATGCTTAACCTGATCCTGTTGATGCTTCTGAATAGAAAT 1292
 QY 1225 AAGTGGGTTTCCCTGAGAGT 1246
 DB |||||
 DB 1293 AAGTGGGTTTCCCTGAGAGT 1314

RESULT 7
 ADS71344
 ID ADS71344 standard; DNA; 1322 BP.
 XX
 AC ADS71344;
 XX
 DT 16-DEC-2004 (First entry)
 XX
 XX
 DE Human l1vin alpha splice variant DNA.
 XX
 XX Immune response; cancer-associated inhibitor of Apoptosis-family protein;
 KW IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma;
 KW human; l1vin alpha; gene; de; immunostimulant; cytostatic.

```

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 174..1070
XX FT /tag= a
XX FT /product= "Human livin alpha splice variant protein"
XX
XX PN US2004192631-A1.
XX PD 30-SEP-2004.
XX PF 24-MAR-2004; 2004US-00807897.
XX PR 24-MAR-2003; 2003US-0457009P.
XX PA (XIAN/) XIAN R.
XX PA (ZHOU/) ZHOU H.
XX PA (REIS/) REISEFELD R A.
XX PI Xiang R, Zhou H, Reisfeld RA;
XX
XX DR WPI; 2004-689881/67.
XX DR P-PSDB; ADS71345.
XX DR REFSO; NM_139317.
XX
XX PT New DNA vaccine comprising a cancer-associated inhibitor of Apoptosis-
XX PT family protein immunosuppressive gene product, useful for eliciting an immune
XX PT response against cancer.
XX PS Claim 26; SEQ ID NO 26; 84bp; English.
XX
XX CC The present invention relates to a DNA vaccine effective for eliciting an
XX CC immune response against cancer cells which comprises a DNA construct
XX CC operably encoding at least one cancer-associated inhibitor of Apoptosis-
XX CC family protein (IAP-family protein) and at least one immunosuppressive
XX CC product in a pharmaceutical carrier. The invention is useful for treating
XX CC cancer such as lung cancer, colorectal cancer and melanoma. The present
XX CC sequence is the human livin alpha splice variant DNA.
XX
XX SQ Sequence 1322 BP; 212 A; 417 C; 445 G; 248 T; 0 U; 0 Other;
XX
XX Query Match 93.4%; Score 1164; DB 13; Length 1322;
XX Best Local Similarity 95.8%; Pred. No. 2.5e-246;
XX Matches 1228; Conservative 0; Mismatches 0; Indels 54; Gaps 1;
XX
XX QY 19 GGCAGGCTGTGCTATCCCTGCTGCTCCCAAGGTGGGCCCGGGGGTACAGAGCTCCAG 78
XX DB 33 GGCAGGCTGTGCTATCCCTGCTGCTCCCAAGGTGGGCCCGGGGGTACAGAGCTCCAG 92
XX
XX QY 79 AAGGGGACAGCTGGGCAATTATTTGAGATTGGCCATCAGCCCCCAATTTCTGCTCAAACTCG 138
XX DB 93 AAGGGGACAGCTGGGCAATTATTTGAGATTGGCCATCAGCCCCCAATTTCTGCTCAAACTCG 152
XX
XX QY 139 GTCCAGAGCCAGTGTTCCTTCATGGGACCTTAAAGACAGTGGCCAGAGCTTCGACCGTGA 198
XX DB 153 GTCCAGAGCCAGTGTTCCTTCATGGGACCTTAAAGACAGTGGCCAGAGCTTCGACCGTGA 212
XX
XX QY 199 CCACAGCCGAGCCACTGGGACGCGGTGATGCTCCACGACAGACGCGTGTGACCCCGC 258
XX DB 213 CCACAGCCGAGCCACTGGGACGCGGTGATGCTCCACGACAGACGCGTGTGACCCCGC 272
XX
XX QY 259 TCTCTGGGAGGCGCTGTCTAGGCTGAGCACTTCAGACAGCTTCGGACCACTGATGGG 318
XX DB 273 TCTCTGGGAGGCGCTGTCTAGGCTTCAGACACTTCAGACAGCTTCGGACCACTGATGGG 332
XX
XX QY 319 CAGATCTTGGGCGCACTGGGCGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
XX DB 333 CAGATCTTGGGCGCACTGGGCGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
XX
XX QY 379 ACCTGTCCAGGGGAGGAGCTGCTTCCCGGCACTGGGCTTGAAGAGTTCGCTGCTCC 438
XX DB 393 ACCTGTCCAGGGGAGGAGCTGCTTCCCGGCACTGGGCTTGAAGAGTTCGCTGCTCC 452

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QY 439 TTCTATGACTGGCCGCTGACTGCTGAGAGTTCACACCCAGCTGCTGCTCCGAGCTTC 498
DB 453 TTCTATGACTGGCCGCTGACTGCTGAGAGTTCACACCCAGCTGCTGCTCCGAGCTTC 512
QY 499 TTCCACACAGGCGCATCAGAGCAAGGTGAGTGTCTTCTGCTATGAGGGGAGCTGAGAGC 558
DB 513 TTCCACACAGGCGCATCAGAGCAAGGTGAGTGTCTTCTGCTATGAGGGGAGCTGAGAGC 572
QY 559 TGGAAAGCGGGGAGAGAGAGCCCTGGAACGAGACATGCAAGTGTTCCTCCAGCTGCAATTTC 618
DB 573 TGGAAAGCGGGGAGAGAGAGCCCTGGAACGAGACATGCAAGTGTTCCTCCAGCTGCAATTTC 632
QY 619 CTGCTCCGCTCAAAAGAGAGAGAGCTTGTTCACAGATGTGACAGAGAGAGAGAGAGAGAG 678
DB 633 CTGCTCCGCTCAAAAGAGAGAGAGCTTGTTCACAGATGTGACAGAGAGAGAGAGAGAGAG 692
QY 679 CTGAGCTCCTGAGAGAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738
DB 693 CTGAGCTCCTGAGAGAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 752
QY 739 CTGCTCCTGAGAGAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 798
DB 753 CTGCTCCTGAGAGAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 812
QY 799 CAGAG----- 804
DB 813 CAGAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 872
QY 805 CCAGAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 864
DB 873 CCAGAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 932
QY 885 GTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 924
DB 933 GTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 992
QY 925 GAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 984
DB 993 GAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1052
QY 985 GGCACCTTCTGCTCTTGAAGGCGAGGTGCGATGCGCGGCGAGGTGGTGGAGAGTGGGCTC 1044
DB 1053 GGCACCTTCTGCTCTTGAAGGCGAGGTGCGATGCGCGGCGAGGTGGTGGAGAGTGGGCTC 1112
QY 1045 CTTGCGCCCTCTTGAAGGCGAGGTGCGATGCGCGGCGAGGTGGTGGAGAGTGGGCTC 1104
DB 1113 CTTGCGCCCTCTTGAAGGCGAGGTGCGATGCGCGGCGAGGTGGTGGAGAGTGGGCTC 1172
QY 1105 TGTTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1164
DB 1173 TGTTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1232
QY 1165 CCTTGTCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1224
DB 1233 CCTTGTCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1292
QY 1225 AAGTGGGATTTTCCCTGAGAGT 1246
DB 1293 AAGTGGGATTTTCCCTGAGAGT 1314

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RESULT 8
 ID AA261210 standard; DNA; 1337 BP.
 XX AA261210;
 AC
 XX 30-MAY-2000 (first entry)
 DT
 XX DNA encoding a human inhibitor of apoptosis protein (HIAP3).
 DE
 XX Human, inhibitor of apoptosis protein; HIAP3; apoptosis; cancer;
 KW

XX cDNA encoding a human proliferation and apoptosis related protein.
 DE Human; proliferation and apoptosis related protein; PROAP; psoriasis;
 XX cell proliferative disorder; immunological disorder; hepatitis;
 KW reproductive disorder; arteriosclerosis; cirrhosis; lymphoma;
 KW cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia;
 KW asthma; diabetes mellitus; osteoarthritis; endometriosis;
 KW uterine fibroid; menstrual cycle; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 215..1111
 FT CDS /tag= a
 FT /product= "proliferation and apoptosis related protein"
 XX
 XX WO00023589-AZ.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024511.
 XX
 XX 20-OCT-1998; 98US-0172216P.
 PR 04-FEB-1999; 99US-0118559P.
 PR 11-FEB-1999; 99US-0172229P.
 PR 22-APR-1999; 99US-0154336P.
 XX
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Tang YT, Yue H, Hillman JL, Guegler KJ, Corley NC, Lal P;
 PI Azimzal Y, Baughn MR, Yang J, Shih LI;
 XX WPI: 2000-339688/29.
 DR P-PSDB; AAY84907.
 XX
 XX New human proliferation and apoptosis related protein polypeptides used
 PT for diagnosis, treatment and prevention of cell proliferative,
 PT immunological and reproductive disorders.
 XX
 PS Claim 9; Page 121; 128pp; English.
 XX
 XX The present sequence encodes a human proliferation and apoptosis related
 CC protein (PROAP). The polypeptides and polynucleotides can be used for the
 CC diagnosis, treatment and prevention of cell proliferative, immunological
 CC and reproductive disorders. Disorders associated with decreased
 CC expression or activity of include arteriosclerosis, cirrhosis, hepatitis,
 CC psoriasis, melanoma, lymphoma and cancers of the breast, brain and
 CC prostate, acquired immune deficiency syndrome (AIDS), allergies, anaemia,
 CC asthma, diabetes mellitus, osteoarthritis, endometriosis, uterine
 CC fibroids and disruptions of the menstrual cycle. Antibodies against PROAP
 CC can be used in diagnosis of disorders characterized by PROAP e.g. in ELISA
 CC (enzyme linked immunosorbent assays) and the polynucleotides may be used
 CC to detect and quantify gene expression in biopsied tissues. These
 CC techniques can also be used to monitor regulation of PROAP levels during
 CC therapeutic intervention
 XX
 XX Sequence 1363 BP; 228 A; 428 C; 455 G; 252 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 93.0%; Score 1159.4; DB 3; Length 1363;
 XX Best Local Similarity 95.7%; Pred. No. 2,6e-245;
 XX Matches 124; Conservative 0; Mismatches 1; Indels 54; Gaps 1,
 QY 19 GGCAGGCGCTGCTCCCTGCTGCTCCAGGCGGCGCGCGGGGCTCAGAGCTTCAG 78
 Db 74 GGCAGGCGCTGCTCCCTGCTGCTCCAGGCGGCGCGCGGGGCTCAGAGCTTCAG 133
 QY 79 AAGGCGCAGCTGGGCAATATTCGAGATTGGCCATGAGCCCATTTCTGCTGCAAACTG 138
 Db 134 AAGGCGCAGCTGGGCAATATTCGAGATTGGCCATGAGCCCATTTCTGCTGCAAACTG 193
 QY 139 GTCAGAGCAGGTGCTCCCTCCATGGAGCTTAAGCACTGCCAAGTGCCTGACCGTGA 198
 |||

Db 194 GTCAGAGCAGGTGCTCCCTCCATGGGCGCTAAAGACAGTGCACAGTGCCTGACCGTGA 253
 QY 199 CCACAGCGGACCACTGGGAGCGGGTGAATGGTCCACACAGAGAGGCTGTGACCCCGC 258
 Db 254 CCACAGCGGACCACTGGGAGCGGGTGAATGGTCCACACAGAGAGGCTGTGACCCCGC 313
 QY 259 TCTCTGGGCAAGCTGTCTTGAAGCTTGAACACTGTCAGAGCTGTGGACACAGTGAATGG 318
 Db 314 TCTCTGGGCAAGCTGTCTTGAAGCTTGAACACTGTCAGAGCTGTGGACACAGTGAATGG 373
 QY 319 CAGATCCTGGGCAAGCTGTGGGCGCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
 Db 374 CAGATCCTGGGCAAGCTGTGGGCGCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 433
 QY 379 ACCCTGTCCAGGGGCGCTGCTTCCCGGCAATGGGCTGTGAGAGATTGCTGTGAGCTCC 438
 Db 434 ACCCTGTCCAGGGGCGCTGCTTCCCGGCAATGGGCTGTGAGAGATTGCTGTGAGCTCC 493
 QY 439 TTCTAAGACTGGGCGCTGACTGAGAGTGCACCCGAGCTGTGCTGCGGCTTC 498
 Db 494 TTCTAAGACTGGGCGCTGACTGAGAGTGCACCCGAGCTGTGCTGCGGCTTC 553
 QY 499 TTCACACAGGCGCATCAGGACCAAGGTGAGTGTCTTCTGCTAATGGGGCGCTGAGAGC 558
 Db 554 TTCACACAGGCGCATCAGGACCAAGGTGAGTGTCTTCTGCTAATGGGGCGCTGAGAGC 613
 QY 559 TGGAAAGCGGGGAGACGACCCCTGACGAGAGCATGCCAAGTGTTCGCCAGCTGTCAATTG 618
 Db 614 TGGAAAGCGGGGAGACGACCCCTGACGAGAGCATGCCAAGTGTTCGCCAGCTGTCAATTG 673
 QY 619 CTGCTCCGATCAAAAGAGAGACTTGTCCACAGTGTGACAGAGACTCATCTCCAGCTG 678
 Db 674 CTGCTCCGATCAAAAGAGAGACTTGTCCACAGTGTGACAGAGACTCATCTCCAGCTG 733
 QY 679 CTGGCTCTCTGAGAACCCGTGGAAAGAACCGGAAAGCAGCCCTGTGAGCCCTCCGTC 738
 Db 734 CTGGCTCTCTGAGAACCCGTGGAAAGAACCGGAAAGCAGCCCTGTGAGCCCTCCGTC 793
 QY 739 CTTGCTCTTGGGTACCTGAGAGTGCACACCCAGAGAGAGTGTCAAGTGTGAAGTGC 798
 Db 794 CTTGCTCTTGGGTACCTGAGAGTGCACACCCAGAGAGAGTGTCAAGTGTGAAGTGC 853
 QY 799 CAGAG----- 804
 Db 854 CAGAGCCAGAGAGGAGTCAATCCAGCCGAGGCCCAAGAGGCGTGTGGTCTTGAAGCC 913
 QY 805 CCAAGACCCAGAGAGTGTGAGAGCGCAGCTGCGCGCTGCAAGAGAGAGAGAGAGTGCAG 864
 Db 914 CCAAGACCCAGAGAGTGTGAGAGCGCAGCTGCGCGCTGCAAGAGAGAGAGAGAGTGCAG 973
 QY 865 GTGTGCTTGAACCGCGCGTGTCCATGTCTTGTGTGCGCGGAGCACTGTGTGTGCT 924
 Db 974 GTGTGCTTGAACCGCGCGTGTCCATGTCTTGTGTGCGCGGAGCACTGTGTGTGCT 1033
 QY 925 GAGTGTGCGCGCGCGCTGAGCTGTGCGCATGTGAGAGCCCGTGTGCGAGCCGCGTG 984
 Db 1034 GAGTGTGCGCGCGCGCTGAGCTGTGCGCATGTGAGAGCCCGTGTGCGAGCCGCGTG 1093
 QY 985 CGCACCTCTGTCCTAAGGCGAGTGCATAGGCGGCGCGAGTGTGAGTGTGAGTGTGCTC 1044
 Db 1094 CGCACCTCTGTCCTAAGGCGAGTGCATAGGCGGCGCGAGTGTGAGTGTGAGTGTGCTC 1153
 QY 1045 CTTGCGCGCTTCTGCTGTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1104
 Db 1154 CTTGCGCGCTTCTGCTGTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1213
 QY 1105 TGTTCATCCAGACTGACCAAGCTGTATTCCTGACCAAGCGCCAGAGTGTGAGAGAGAG 1164
 Db 1214 TGTTCATCCAGACTGACCAAGCTGTATTCCTGACCAAGCGCCAGAGTGTGAGAGAGAG 1273
 QY 1165 CCTTGTCTTGGCGTGGGAGTGGCTTAATGTGACCTGTGTGTGTGTGTGTGTGTGTGTGT 1224
 Db 1274 CCTTGTCTTGGCGTGGGAGTGGCTTAATGTGACCTGTGTGTGTGTGTGTGTGTGTGTGT 1333

Qy	1225	AAAGTGGGTTTCCCTGGA	1243
Db	1334	AAAGTGGGTTTCCCTGGA	1352

Db 1094 CGCACCCTTCCTGCTAGGCGCAGTGCCATGCGCGGCGGAGGCTGCGAGATGGGCTC 1153
QY 1045 CCTGCCCTCTGCTGCTGTTGGAAGTGTCTTCTGCGCTGCTGGAAGATGGCAAGCTGG 1104
Db 1154 CCTGCCCTCTGCTGCTGTTGGAAGTGTCTTCTGCGCTGCTGGAAGATGGCAAGCTGG 1213
QY 1105 TGTTCATCCAGCAGTACGACGCTGATTCCTCCGACGACCGCGGAGTGGAGAAGAGG 1164
Db 1214 TGTTCATCCAGCAGTACGACGCTGATTCCTCCGACGACCGCGGAGTGGAGAAGAGG 1273
QY 1155 CCTTGTGCTGGGCTGGGAGATGGCTTAAGTACTGTTTGGATGCTTCTGAATAGAAT 1224
Db 1274 CCTTGTGCTGGGCTGGGAGATGGCTTAAGTACTGTTTGGATGCTTCTGAATAGAAT 1333
QY 1225 AAGTGGGTTTCCCTGGA 1243
Db 1334 AAGTGGGTTTCCCTGGA 1352

RESULT 11
ADH89543
ID ADH89543 standard; DNA; 1168 BP.
XX
AC ADH89543;
XX
DT 22-APR-2004 (first entry)
XX
DE Human livin genomic DNA #2.
XX
KW hyperproliferative disorder; aberrant apoptosis; human; ds; livin; gene.
XX
OS Homo sapiens.
XX
PN US2004005565-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00186646.
XX
PR 02-JUL-2002; 2002US-00186646.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Doble KW;
XX
DR WPI; 2004-098436/10.
XX
DR P-PSDB; ADH89686.
XX
PT New antisense oligonucleotide, having a sequence targeted to a nucleic
PT acid encoding livin, useful for preparing a composition for treating
PT hyperproliferative disorder or aberrant apoptosis.
XX
PS Example 15; SEQ ID NO 12; 60pp; English.
XX
SS The invention relates to an antisense oligonucleotide targeted to a
CC nucleic acid encoding livin and that specifically hybridises with the
CC nucleic acid encoding livin and inhibits expression of livin. The
CC antisense oligonucleotide is useful for preparing a composition for
CC treating hyperproliferative disorder or aberrant apoptosis. The present
CC sequence represents human livin DNA.
SQ Sequence 1168 BP; 206 A; 357 C; 393 G; 212 T; 0 U; 0 Other;

Query Match 82.0%; Score 1021.4; DB 12; Length 1168;
Best Local Similarity 95.2%; Pred. No. 5.9e-215;
Matches 1086; Conservative 0; Mismatches 1; Indels 54; Gaps 1;
QY 160 ATGGGACCTTAAGACAGTGCCTGACCGTGGACCAAGCCGAGCACTGGGCA 219
Db 1 ATGGGACCTTAAGACAGTGCCTGACCGTGGACCAAGCCGAGCACTGGGCA 60
QY 220 GCGGATGATGCTCCACGAGAGGCTGTGAGCCCGCTCTTGGGAGGCGTGTCTTA 279

Db 61 GCGGATGATGCTCCACGAGAGGCGTGTGAGACCCCGCTCTGTGGGAGGCCCTGTCTTA 120
QY 280 GGCCTGAGACCTTGACAGAGCTTGGAGCAAGTGTGATGGGCAATCTGGGAGCAAGCTGGG 339
Db 121 GGCCTGAGACCTTGACAGAGCTTGGAGCAAGTGTGATGGGCAATCTGGGAGCAAGCTGGG 180
QY 340 CCCCTGACAGAGAGAGAGAGAGAGAGGCGCGGAGCCACTTGTCCAGAGGGGCGCTGCC 399
Db 181 CCCCTGACAGAGAGAGAGAGAGAGAGGCGCGGAGCCACTTGTCCAGAGGGGCGCTGCC 240
QY 400 TTCCCGGAGATGGGCTTGAAGAGTGGCTTGGCTCTCTTGAATGACTGGCGGTGAAT 459
Db 241 TTCCCGGAGATGGGCTTGAAGAGTGGCTTGGCTCTCTTGAATGACTGGCGGTGAAT 300
QY 460 GCTGAGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
Db 301 GCTGAGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 520 AAGTGAAGTGTCTTCTTCTGCTATGAGGAGCTGACAGACTGGAAGCGGAGGAGACCCC 579
Db 361 AAGTGAAGTGTCTTCTTCTGCTATGAGGAGCTGACAGACTGGAAGCGGAGGAGACCCC 420
QY 580 TGAAGGAGCATGCCAAGTGTTCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
Db 421 TGAAGGAGCATGCCAAGTGTTCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 640 GACTTGTTCACAGTGTGACAGAGAGCTGACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
Db 481 GACTTGTTCACAGTGTGACAGAGAGCTGACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 700 GAAGAAGCGGAG 759
Db 541 GAAGAAGCGGAG 600
QY 760 CTGCCACACCCAG 804
Db 601 CTGCCACACCCAG 660
QY 805 -----CGAGAGCCAGAGATGTGAG 825
Db 661 CGAGCCAGAGCCAG 720
QY 826 GCGAGCTGCGGCGGCTGACAG 885
Db 721 GCGAGCTGCGGCGGCTGACAG 780
QY 886 TCCATCGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 945
Db 781 TCCATCGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 946 CTGAGCCCATCTGACAG 1005
Db 841 CTGAGCCCATCTGACAG 900
QY 1006 AGGTGACATGAGCGGAG 1065
Db 901 AGGTGACATGAGCGGAG 960
QY 1066 TGAAGTGTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1125
Db 961 TGAAGTGTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1126 CCTGATTCCTCCGACAG 1185
Db 1021 CCTGATTCCTCCGACAG 1080
QY 1186 GGTCTTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1245
Db 1081 GGTCTTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1246 T 1246
Db 1141 T 1141

XX 25-APR-2002.
 PD 16-OCT-2001; 2001WO-JP009071.
 PF 17-OCT-2000; 2000JP-00316721.
 PR 20-DEC-2000; 2000JP-00386809.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX Tanaka H, Kajeda I;
 PI WPI: 2002-435536/46.
 DR P-PSDB; AA014947.
 XX
 XX Baculovirus iAP repeat domain or RING-finger domain-containing survivin-
 PT like polypeptides and encoded DNA, applicable in diagnosis and screening
 XX compounds for treating various cancers and apoptosis abnormality.
 PS Disclosure; Page 122; 136pp; Japanese.
 CC The invention comprises the amino acid and coding sequences of survivin-
 CC like proteins. The survivin-like DNA and protein sequences are useful in
 CC diagnostics and screening compounds for treating various cancers and
 CC apoptosis abnormality, including gene therapy. The present DNA sequence
 CC encodes a survivin-like protein or the invention
 XX
 SQ Sequence 840 BP; 136 A; 272 C; 287 G; 144 T; 0 U; 1 Other;
 Query Match 67.3%; Score 838; DB 6; Length 840;
 Best Local Similarity 99.8%; Pred. No. 1.3e-174;
 Matches 838; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 160 ATGGGACCTTAAGACAGTGGCCCAAGTGCCTGACCCGTGACACAGCCGAGCCCACTGAGCA 219
 DB 1 ATGGAGCCCTTAAGACAGTGGCCCAAGTGCCTGACCCGTGACACAGCCGAGCCCACTGAGCA 60
 QY 220 GCCGGTATGATGTCCTCAAGCAGAGCGCTGTGGAACCCCGCTCTCTGGGCAAGCCTGTCTTA 279
 DB 61 GCCGGTATGATGTCCTCAAGCAGAGCGCTGTGGAACCCCGCTCTCTGGGCAAGCCTGTCTTA 120
 QY 280 GGCTTGAACACTGTCAGAGCCTTGGAGACCACTGATGAGGAGATCTCTGGGCAAGCCTGTCTTA 339
 DB 121 GGCTTGAACACTGTCAGAGCCTTGGAGACCACTGATGAGGAGATCTCTGGGCAAGCCTGTCTTA 180
 QY 340 CCCCTGACAGAGGAG 399
 DB 181 CCCCTGACAGAGGAG 240
 QY 400 TTCCCGGCAATGAGGCTCTTGAAGAGTTCCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 459
 DB 241 TTCCCGGCAATGAGGCTCTTGAAGAGTTCCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 QY 460 GCTGAGGTGTCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
 DB 301 GCTGAGGTGTCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 520 AAGGTGAGGTCTTCTTCTGCTATGAGGAGCTGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 579
 DB 361 AAGGTGAGGTCTTCTTCTGCTATGAGGAGCTGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 420
 QY 580 TGAACGAGAGTTCACAGTGTTCCTCCAGCTGTCAAGTTCCTGCTCCGCTCAAAAGAGAGA 639
 DB 421 TGAACGAGAGTTCACAGTGTTCCTCCAGCTGTCAAGTTCCTGCTCCGCTCAAAAGAGAGA 480
 QY 640 GACTTGTCTCACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTCTGAGTACCCCTGAG 699
 DB 481 GACTTGTCTCACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTCTGAGTACCCCTGAG 540
 QY 700 GAAAGAACGGAAGACGACGAGCCCTGTGAGCCCTCTCCCTGCTCTGAGTACCCCTGAG 759
 DB 541 GAAAGAACGGAAGACGACGAGCCCTGTGAGCCCTCTCCCTGCTCTGAGTACCCCTGAG 600

QY 760 CTGCCCAACCCAGAGAGAGGTCCAGTCTGAAAGTGCCTCAGAGGCTCAGAGGAGAGAT 819
 DB 601 CTGCCCAACCCAGAGAGAGAGGTCCAGTCTGAAAGTGCCTCAGAGGCTCAGAGGAGAT 660
 QY 820 GTGGAGAGCCAGTGTGCGGCGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
 DB 661 GTGGAGAGCCAGTGTGCGGCGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 880 GCCGTGTCAATGCTTTTGTGCGGCGAGCACTGTGTGTCAGAGTGTGCGGCGAGC 939
 DB 721 GCCGTGTCAATGCTTTTGTGCGGCGAGCACTGTGTGTCAGAGTGTGCGGCGAGC 780
 QY 940 CTGCACTGTGCCCCATCTGCAAGAGCCCGTCCAGAGCCGAGTGTGAGCACTTCTGTCC 999
 DB 781 CTGCACTGTGCCCCATCTGCAAGAGCCCGTCCAGAGCCGAGTGTGAGCACTTCTGTCC 840
 RESULT 14
 AAS91553
 ID AAS91553 standard; cDNA; 3782 BP.
 XX
 XX AAS91553;
 AC
 DT 13-FEB-2002 (first entry)
 XX
 XX
 DE DNA encoding novel human diagnostic protein #27357.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW Food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2001/5067-A2.
 PN
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HSE-) HXSEQ INC.
 PA
 PI Drmanac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 DR P-PSDB; ABG27366.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensic, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PT
 XX
 PS Claim 1; SEQ ID NO 27357; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensic, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

Sequence 3782 BP, 656 A, 1127 C, 1215 G, 716 T, 0 U, 68 Other;

Query Match 58.6%; Score 729.8; DB 5; Length 3782;
 Best Local Similarity 79.6%; Pred. No. 1.1e-150;
 Matches 1033; Conservative 0; Mismatches 2; Indels 262; Gaps 4;

QY 140 TCAGAGCCAGTGTTCCTTCATGAGACCTTAAGACATGAGCCCAAGTGCCTGCACCGTGCAC 199
 DB TCAGAGCCAGTGTTCCTTCATGAGACCTTAAGACATGAGCCCAAGTGCCTGCACCGTGCAC 2239
 QY 200 CACAGCCGAGCCATGAGGACGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 259
 DB CACAGCCGAGCCATGAGGACGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2299
 QY 260 CTCTGGGACGCGCTGTCTAGGCTTGAACCTGACAGGCTGGGACCACTGATGATGATGATGAT 319
 DB CTCTGGGACGCGCTGTCTAGGCTTGAACCTGACAGGCTGGGACCACTGATGATGATGATGAT 2359
 QY 320 AGATCTGGGACGCGCTGTCTAGGCTTGAACCTGACAGGCTGGGACCACTGATGATGATGATGAT 379
 DB AGATCTGGGACGCGCTGTCTAGGCTTGAACCTGACAGGCTGGGACCACTGATGATGATGATGAT 2419
 QY 380 CCTGTGTCAGGAGGCGCTGCTTCCCGGACATGAGGCTGTAAGAGATGATGATGATGATGATGAT 439
 DB CCTGTGTCAGGAGGCGCTGCTTCCCGGACATGAGGCTGTAAGAGATGATGATGATGATGATGAT 2420
 QY 440 TCTATGACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499
 DB TCTATGACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2539
 QY 500 TCCACACA----- 507
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 XX DT 19-NOV-2001 (first entry)
 XX DE Human SBH80014. IAPA gene #2.
 XX KW Human; Alzheimer's disease; amyotrophic lateral sclerosis; ALS;
 KW Zollinger-Ellison syndrome; immune system disease; schizophrenia;
 KW inflammation; haematopoietic disease; anxiety; feeding disorder; aging;
 KW anorexia; depression; cardiovascular disease; sleep disorder; seizure;
 KW memory alteration; migraine; stroke; asthma; neuropathy; hypoglycemia;
 KW sexual disorder; growth abnormality; infection; autoimmune disease;
 KW rheumatoid arthritis; cataractogenesis; angiogenesis; Hodgson's disease;
 KW cerebral ischaemia; cirrhosis; Huntington's disease; diabetes disease;
 KW hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity;
 KW diabetes mellitus; glomerulonephritis; renovascular hypertension; cancer;
 KW vaccine; gene therapy; SBH80014. IAPA gene; ds.
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 XX FH Key Location/Qualifiers
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 FT /note= "CDS does not include stop codon"
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 XX PD 23-AUG-2001.
 XX PF 14-FEB-2001, 2001MO-US004703.
 XX PR 14-FEB-2000, 2000US-0182172P.
 XX PR 29-FEB-2000, 2000US-0186084P.
 XX PR 18-APR-2000, 2000US-0198583P.
 XX PR 04-OCT-2000, 2000US-0237963P.
 XX (SMK) SMITHKLINE BEECHAM CORP.
 XX PA (SMK) SMITHKLINE BEECHAM PLC.
 XX PI Agarwal P, Kabnick KS, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

```

XX WPI: 2001-536566/59.
DR P-PSDB; AAE09458.
XX
XX New secreted and membrane associated polypeptides for treating
PT Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
PT disorders, stroke, and asthma.
XX
PS Claim 2; Page 53; 94pp; English.
XX
CC The present sequence is a gene encoding human SBH80014.IAPA protein, a
CC cytosolic protein of the invention. The invention relates to secreted and
CC membrane associated polypeptides and nucleic acid molecules encoding such
CC polypeptides. Sequences of the invention are useful for treating diseases
CC such as Alzheimer's disease, amyotrophic lateral sclerosis (ALS),
CC Zollinger-Ellison syndrome, diseases of the immune system, haematopoietic
CC disease, inflammation, anxiety, schizophrenia, feeding disorders,
CC anorexia, depression, social, sexual and rewarded behaviour,
CC cardiovascular disease, sleep disorder, learning and memory alteration
CC and altered immune response, seizure, migraine, cancer, stroke, asthma,
CC neuropathy, aging, sexual disorders, treatment of transsexuals, growth
CC abnormalities, obesity, infections, autoimmune diseases (e.g. rheumatoid
CC arthritis), cataractogenesis, angiogenesis, disorders associated with
CC healthy maintenance of gastric mucosa and repair of acute and chronic
CC mucosal lesion, lung carcinoma, cerebral ischaemia, atherosclerosis,
CC cirrhosis, Huntington's disease, headache, amnesia, multiple sclerosis,
CC Hodgson's disease, dilated cardiomyopathy, congestive heart failure,
CC cardiac arrhythmias, hypercholesterolaemia, viral and non-viral
CC hepatitis, type I and type II diabetes mellitus, glomerulonephritis,
CC renovascular hypertension, hypoglycaemia, periodic paralyses, tendinitis
CC and malignant hyperthermia. Polypeptides of the invention are used to
CC identify membrane bound and soluble receptors. They are also useful as
CC vaccines for inducing an immunological response in a mammal.
CC Polynucleotides of the invention are used in gene therapy. They are also
CC valuable for chromosome localisation studies and tissue expression
CC studies
XX
SQ Sequence 769 BP; 122 A; 248 C; 265 G; 134 T; 0 U; 0 Other;
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Query Match 54.2%; Score 675; DB 4; Length 769;
Best Local Similarity 91.2%; Pred. No. 9.1e-139;
Matches 769; Conservative 0; Mismatches 0; Indels 74; Gaps 2;
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DB 61 GCCGGTGTATGGTCCCAACGACAGACCGCTGTGACCCCGCTCTTGGGACAGCCCTGTCTTA 120
QY 280 GGCCTTGACACCTGGACAGAGCTTGGACACAGTGGATGGGACAGATCCTTGGCCAGCTGGCG 339
DB 121 GGCCTTGACACCTGGACAGAGCTTGGACACAGTGGATGGGACAGATCCTTGGCCAGCTGGCG 180
QY 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
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QY 460 GCTGAGGTGCGACCCGAGCTGTGCTGTGCTGCTGCTGCTTCTTCCACAGAGCCATCAGGAC 519
DB 301 GCTGAGGTGCGACCCGAGCTGTGCTGTGCTGCTGCTTCTTCCACAGAGCCATCAGGAC 360
QY 520 AAGGTGAGGTGCTTCTTCTGCTATGAGGAGCTGACAGAGTGGAGAGCGAGGAGAGAGAGAG 579
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DB 647 GCGTGTCCATGTCTTTGTGTGCGCGGACACCTGTGTGTGTGAGTGTGCCCGCGC 706
QY 940 CTGACAGTGTGCCCATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
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QY 1000 TAG 1002
DB 767 TAG 769

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Search completed: April 19, 2006, 21:57:04
Job time : 854 secs

QY	199	CCAAGCCGAGCCCACTGGGAGCCGGTGAATGTCCACGAGAGCCCTGTGAGCCCGC	258
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QY	259	TCTCTGGGCAAGCCCTGTCTTAAGGCTGTGAGACACCTGGAGACCTTGGAGACACGTGATGG	318
Db	273	TCTCTGGGCAAGCCCTGTCTTAAGGCTGTGAGACACCTGGAGACACGTGATGG	332
QY	319	CAGATCTTGGGCAAGCTTGGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAG	378
Db	333	CAGATCTTGGGCAAGCTTGGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAG	392
QY	379	ACCTTGTCCAGGGGGGCCCCCTTCCCCGGGATAGGGCTCTTGAAGAGTTGCTTGGCCCTCC	438
Db	393	ACCTTGTCCAGGGGGGCCCCCTTCCCCGGGATAGGGCTCTTGAAGAGTTGCTTGGCCCTCC	452
QY	439	TTCTATAGACTGGCGCGTGACTGTGTAGAGTCCACCCGAGCTGTGGCTGTGCGCGGCTTC	498
Db	453	TTCTATAGACTGGCGCGTGACTGTGTAGAGTCCACCCGAGCTGTGGCTGTGCGCGGCTTC	512
QY	499	TTCCACACAGGCCATCAGGACAGAGGTGAGGTCTTCTTCTGCTATAGGGGGCTTCGAGAGC	558
Db	513	TTCCACACAGGCCATCAGGACAGAGGTGAGGTCTTCTTCTGCTATAGGGGGCTTCGAGAGC	572
QY	559	TGGAAGGCGGGGAGACGACCCCTGAGCGAGACATGCCAAGTGTTTCCCAAGCTGTGACCTTC	618
Db	573	TGGAAGGCGGGGAGACGACCCCTGAGCGAGACATGCCAAGTGTTTCCCAAGCTGTGACCTTC	632
QY	619	CTGTCTCCGGTCAAAAGAGAGAGACTTTGTTCACAGTGTGCAAGAGACACTACTCCAGCTG	678
Db	633	CTGTCTCCGGTCAAAAGAGAGAGACTTTGTTCACAGTGTGCAAGAGACACTACTCCAGCTG	692
QY	679	CTGGGCTCTGGGAGCCCGTGGGAAAGAACGGGAAGACGGACCCCTGTGGCCCCCTTCCTTC	738
Db	693	CTGGGCTCTGGGAGCCCGTGGGAAAGAACGGGAAGACGGACCCCTGTGGCCCCCTTCCTTC	752
QY	739	CCTGCTCTGGGTAACCTTGAAGCTGCCACACCCAGAGAGAGATCCAGTCTGAAAGTGCC	798
Db	753	CCTGCTCTGGGTACCTTGAAGCTGCCACACCCAGAGAGAGATCCAGTCTGAAAGTGCC	812
QY	799	CAGGAGCCGAGAGCCAGGAGATGTGAGAGGCGACCTGGCGGGCTGCAGAGAGAGAGACG	858
Db	813	CAGGAGCCGAGAGCCAGGAGATGTGAGAGGCGACCTGGCGGGCTGCAGAGAGAGAGACG	872
QY	859	TGCCAAGTGTGCTGTGACCGGCGCGTGTCACTGATCTTGTGTCGGTGGGCCACCTGGTTC	918
Db	873	TGCCAAGTGTGCTGTGACCGGCGCGTGTCACTGATCTTGTGTCGGTGGGCCACCTGGTTC	932
QY	919	TGTGTGATGTGCCCCCGGCGCTGCAAGCTGTGCCCCATCTGACAGACCCTGTGCGAGCC	978
Db	933	TGTGTGATGTGCCCCCGGCGCTGCAAGCTGTGCCCCATCTGACAGACCCTGTGCGAGCC	992
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QY	1159	AGGAGGCCCTTGTGTCGTGCGTGGGGATAGGCTTAATGATCACTGTTTGGATGCTTCTGAAT	1218
Db	1173	AGGAGGCCCTTGTGTCGTGCGTGGGGATAGGCTTAATGATCACTGTTTGGATGCTTCTGAAT	1232
QY	1219	AGAAATAAGGGGTTTTCCTGTGAGGT 1246	
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LOCUS	CS113085	1260 bp	DNA	linear	PAT 24-JUN-2005
DEFINITION	Sequence 103 from Patent WO2005054507.				
ACCESSION	CS113085				
VERSION	CS113085.1	GI:66224657			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
JOURNAL	1				
FEATURES	Corfe, B. and Chirakkal, H.				
source	Gene screen				
	Patent: WO 2005054507-A 103 16-JUN-2005;				
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QY	259	TCTGTGGGCAAGCCCTGTCTTAGGCGCTGGAACACTGTGAGAGCGCTGGGACCAAGTGAATGGG	318		
DB	273	TCTGTGGGCAAGCCCTGTCTTAGGCGCTGGAACACTGTGAGAGCGCTGGGACCAAGTGAATGGG	332		
QY	319	CAGATCTCTGGGCCAGCTGCGGCCCCCTTGAACAGAGAGAAAGAGAGAGAGGCGCCGGGGCC	378		
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QY	439	TTCTATATACCTGCGCGCTGACTGTGAGGTGACCCCGAGCTTGGCTGCTGCGCGCTTC	498		
DB	453	TTCTATATACCTGCGCGCTGACTGTGAGGTGACCCCGAGCTTGGCTGCTGCGCGCTTC	512		
QY	499	TTCCACACAGGCGCATAGAGACAAGGTGAGAGTCTTCTGTATATGGGGGCGCTGCAAGC	558		
DB	513	TTCCACACAGGCGCATAGAGACAAGGTGAGAGTCTTCTGTATATGGGGGCGCTGCAAGC	572		
QY	559	TGGAAGCGCGGGGACGACCCCTGAGACGAGACATGGCAAGTGGTTCCTCCAGCTGCAGTTC	618		
DB	573	TGGAAGCGCGGGGACGACCCCTGAGACGAGACATGGCAAGTGGTTCCTCCAGCTGCAGTTC	632		
QY	619	CTGCTCCGGTCAAAAGAGAGACTTTGTTCACATGTGTGACAGAGACTCATCTCCAGCTG	678		
DB	633	CTGCTCCGGTCAAAAGAGAGACTTTGTTCACATGTGTGACAGAGACTCATCTCCAGCTG	692		
QY	679	CTGGGCTCTCTGGGACCCGCTGGAGAAACCGGAAGACGAGGCGCTGTGGGCGCCCTGCTG	734		

Db	693	CTGGGCTCCTGGAGACCCCGTGGGAABACCAGAAAGACGAGGCCCTGTGGCCCCCTCCGTC	752
OY	739	CCTGCCTCTGGGTTACCTTGAGCTGCCACAACCAGAAGAGAGTCCAAGCTTGAAAGTGCC	798
Db	753	CCTGCCTCTGGGTAACCTTAGAGCTGCCACAACCAGAAGAGAGTCCAAGCTTGAAAGTGCC	812
OY	799	CAGAGGCCAAGAGCAAGGATGTGGAGGCGAGACTGGCCGGCTGTCAGAGAGAGAGAGAC	858
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OY	859	TGCAAGTGTGTGCTGSAACGCGCCGTGTCATCATGTTTGTGSCGTGGGCAACTGGTC	918
Db	873	TGCAAGTGTGTGCTGSAACGCGCCGTGTCATCATGTTTGTGSCGTGGGCAACTGGTC	932
OY	919	TGTGCTGAGTGTGCCCCCGGCGCTGAGCTGTGCCCCATCTGCAGAGCCCCGTCGACGC	978
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OY	1219	AGAAATAAGTGGGTTTTCCCTGGAGGT	1246
Db	1233	AGAAATAAGTGGGTTTTCCCTGGAGGT	1260
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DEFINITION	Homo sapiens livin inhibitor-of-apoptosis (LIVIN) mRNA, complete cde.		
ACCESSION	AFJ11388		
VERSION	AFJ11388.1	GI:11245452	
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 1260) Kasof,G.M. and Gomes,B.C. Livin, a novel inhibitor of apoptosis protein family member J. Biol. Chem. 276 (5), 3238-3246 (2001)		
AUTHORS	J. Biol. Chem. 276 (5), 3238-3246 (2001)		
TITLE	11024045		
JOURNAL	2 (bases 1 to 1260) Kasof,G.M. and Gomes,B.C. Direct Submision Submitted (05-OCT-2000) Enabling Science and Technology, Asitaneena Pharmaceuticals, 1800 Concord Pike, Wilmington, DE 19803, USA		
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RESULT 4
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ACCESSION AY358835.1 GI:37182787
VERSION AY358835.1
KEYWORDS Full cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1301)
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currali,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,J., Liao,D., Mark,M., Robble,R., Sanchez,C., Schoenfeld,J., Seahagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wiand,D., Woods,K., Xie,M.H., Yaneura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL PubMed 12975309
PUBMED 12975309
REFERENCE 2 (bases 1 to 1301)
Clark,H.F.
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

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Db 134 AAGGCCAGCTGGGCAATTTCTGAGATTGGCCATCAGCCCCCATTTCTGTGCAAACTTG 193
QY 139 GTGAGAGCAGGTGTCCTCATGGGACCTTAAGAAGTGCACAGTGTGCTGCAACCTTGA 198
Db 194 GTGAGAGCAGGTGTCCTCATGGGACCTTAAGAAGTGCACAGTGTGCTGCAACCTTGA 253
QY 199 CCACAGCCGAGCCACTGGGACCGCGATGATGTCGCCACGACGAGCGCTGTGACCCCGC 258
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ACCESSION	AX067715		
VERSION	AX067715.1		GI:12329602
KEYWORDS			
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE			
AUTHORS	Gomes, B. C., Kasof, G. M. and Prosser, J. C.		
TITLE	Livin, inhibitor-of-apoptosis protein-3 (Iap-3)		
JOURNAL	Patent: WO 0077201-A 1 21-DEC-2000;		
	AstraZeneca AB (SE)		
FEATURES			
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	location/Qualifiers		
	organism="Homo sapiens"		
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Query Match	98.6%;	Score 1228;	DB 6; Length 1376;
Best Local Similarity	100.0%;	Pred. No. 3,7e-215;	
Matches 1228;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	19	GGCAGGCTGTGCTTATCTCTGTGCTGCCAGGGTGGGCCCGGGGGTCAGAGCTCCAG	78
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QY	79	AAGGCGCAGCTGGGCGATATTCTGAGATTGGCCATCAGGCCCCCATTTTCTGTCAAACTG	138
Db	130	AAGGCGCAGCTGGGCGATATTCTGAGATTGGCCATCAGGCCCCCATTTTCTGTCAAACTG	189
QY	139	GTCAGAGCAATGTTTCTCTCCATGGAGACTTAAAGCAATGGCCAAAGTGTCTGCACCGTGA	198
Db	190	GTCAGAGCAATGTTTCTCTCCATGGAGACTTAAAGCAATGGCCAAAGTGTCTGCACCGTGA	249
QY	199	CCAAGCGGAGCACTGGGCGAGCGGATGTGGCCAGCAGAGAGCGCTGTGAACCCCGC	258
Db	250	CCAAGCGGAGCACTGGGCGAGCGGATGTGGCCAGCAGAGAGCGCTGTGAACCCCGC	309
QY	259	TCTCTGGGCAACCTGTCTTAGGCTTGACACTGACAGAGCTTGGGACCACTGTGATGGG	318

Db	310	1TCTGGGGAAGCCCTCTGTCTTAGGCTGGACACTGAGCTTGGACCAAGTGGG	369
QY	319	CAGATCTTGGGCGCAGCTGCGGCGCCCTGACAGAGAGAAAGAGAGAGCGCGCGGCGC	378
Db	370	CAGATCTTGGGCGCAGCTGCGGCGCCCTGACAGAGAGAGAAAGAGAGAGCGCGCGGCGC	429
QY	379	ACCTTGTTCAGAGGGGGCTCTGCTTCCCGGCAATGGGCTCTGAGGAATTTGGCTTGGCCTTC	438
Db	430	ACCTTGTTCAGAGGGGGCTCTGCTTCCCGGCAATGGGCTCTGAGGAATTTGGCTTGGCCTTC	489
QY	439	TTCTATGACTGAGCGCGCTGACTGCTGAGGTGACACCGAGCTGCTGGCTGCGCGCTTC	498
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QY	499	TTCCACACAGGCACTACAGACCAAGGTGAGTGTCTTCTGCTATGGGGGCGCTGACAGC	558
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QY	559	TGAAAGCGCGGGAGAGACCCCTCGACGAGACATGCCAGTGTTCCTCCAGCTGTCAATTCC	618
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QY	919	TGTGTGATGTGTGCCCCCGGCGCTTGACGTGTGTGCCCATCTGCAGAGCCCGCTGCCAGC	978
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QY	979	CGCGTGCACACTTCTCTGTCTTAAGCCAGAGTGGCAATGGCCGAGAGGTGGGCTGCAGAGT	1033
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QY	1039	GGGCTCCCTGCGCCCTCTCTGTGCTGTTCGAACTGTGTCTGGGCGCTGTGAGAGATGGCAG	1098
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QY	1159	AGGAGGCGCTTGTCTTGGGTGGGGAGATGGCTTAATCTGTACTGTTTGGATGCTTCTGAAAT	1218
Db	1210	AGGAGGCGCTTGTCTTGGGTGGGGAGATGGCTTAATCTGTACTGTTTGGATGCTTCTGAAAT	1269
QY	1219	AGAAATAAGTGGGTTTTCCTCTGAGAGT 1246	
Db	1270	AGAAATAAGTGGGTTTTCCTCTGAGAGT 1297	

VERSION	CC989690.1	GI:55581892
KEYWORDS		
SOURCE		
ORGANISM	Homo sapiens (human)	
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.	
TITLE	Butz, K., Crnkovic-Mertens, I. and Hoppe-Seyler, F.	
JOURNAL	LIVIN-SPECIFIC AIRRAS FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS	
REFERENCE	Patent: WO 2004091388-A 10 28-OCT-2004; Deutsches Krebsforschungsinstitut Stiftung des oeffentlichen n Rechtes (DS)	
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Best Local Similarity	95.8%;	Pred. No. 26-203;
Matches 1228; Conservative	0; Mismatches	0; Indels 54; Gaps 1;
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Q	Y		1105	TGTCCATCAGACAGTACGACCGCCGTATTCGCCGACACCGCCGAGGGTGGAGAGAGAG	1166
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Q	Y		1165	CCCTTGTCTTGGCGTGGGGAGTGGCTTAACTGTACTGTTTGAATGCTTCTGAATGAAT	1224
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Q	Y		1225	AAAGTGGTTTTTCCCTGGAGGT	1246
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RESULT 7					
BC014475					
LOCUS					
DEFINITION	Homo sapiens baculoviral IAP repeat-containing 7 (IAPIN), transcript variant 1, mRNA (CDNA clone MGC:23131 IMAGE:4859588), complete cds.				
ACCESSION	BC014475				
VERSION	BC014475.1 GI:15680240				
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ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1312) Straussberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Altschul,S.F., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,Y., Hsieh,F., Diatchenko,M., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ushed,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.W., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyshe,S.W., Villalón,D.K., Muzny,D.M., Sodergren,B.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shvachenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schultz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skaleja,U., Smallen,D.E., Scherch,A., Schein,U.E., Jones,S.J. and Marra,M.A.				

TITLE
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED
12477932
REFERENCE
2 (bases 1 to 1312)
AUTHORS
Strauberg, R.
TITLE
Direct Submission
Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DTDP/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Grifflith, Obi Grifflith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska, Diane Smalus, Jeff Stott, Miranda Tsai, George Yang, Jacqie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 34 Row: f Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536419.
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ORIGIN
Query Match 93.4%; Score 1164; DB 8; Length 1312;
Best Local Similarity 95.8%; Pred. No. 2e-203;
Matches 1228; Conservative 0; Mismatches 0; Indels 54; Gaps 1;
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RESULT 8

AY358836 1370 bp mRNA linear PRI 03-OCT-2003

LOCUS Homo sapiens clone DNA172970 LiVIN (UNQ5800) mRNA, complete cds.

ACCESSION AY358836

VERSION AY358836.1 GI:37182789

KEYWORDS FLI_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1370)

Clark,H.P., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brueh,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,O., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Stimmens,L., Singh,J., Smith,V., Slinson,J., Vagstad,A., Vanden,R., Watanabe,C., Wieland,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment

Genome Res. 13 (10), 2265-2270 (2003)

12975309

JOURNAL 2 (bases 1 to 1370)

PUBMED Clark,H.P.

REFERENCE Direct Submission

AUTHORS Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

JOURNAL Location/Qualifiers

FEATURES

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ORIGIN

Query Match 93.4%; Score 1164; DB 8; Length 1370;

Best Local Similarity 95.8%; Pred. No. 2e-203;

Matches 1228; Conservative 0; Mismatches 0; Indels 54; Gaps 1;

Qy 19 GGCAGGCTGTGCTATCCCTGCTGCTCCCAAGGTGGGCCCCGGGGGTCAAGAGCTCCAG 78

Db 74 GGCAGGCTGTGCTATCCCTGCTGCTCCCAAGGTGGGCCCCGGGGGTCAAGAGCTCCAG 133

Qy 79 AAGGGCAGCTGGGCAATATTTGAAGTTGGCCATGAGCCCCCATTTCTGGCAAACTGG 138

Db 134 AAGGGCAGCTGGGCAATATTTGAAGTTGGCCATGAGCCCCCATTTCTGGCAAACTGG 193

Qy 139 GTCAAGGCCAGTGTTCCTCCCACTGGACCTTAAAGAAGTGGCCAGTGCCTGACCGTGA 198

Db 194 GTCAAGGCCAGTGTTCCTCCCACTGGACCTTAAAGAAGTGGCCAGTGCCTGACCGTGA 253

Qy 199 CCACAGCCGAGCCACTGGGCAAGCCGATGGTCCACAGGAGGAGGAGGAGGAGGAGGAGG 258

Db 254 CCACAGCCGAGCCACTGGGCAAGCCGATGGTCCACAGGAGGAGGAGGAGGAGGAGGAGG 313

Qy 259 TCTTGGGCAAGCTGTGCTTGAAGCTTGAACAAGTGGAGGCTGGAGCCAGTGGATGG 318

Db 314 TCTTGGGCAAGCTGTGCTTGAAGCTTGAACAAGTGGAGGCTGGAGCCAGTGGATGG 373

Qy 319 CAGATCCCTGGGCAAGCTGCGGCTTGAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 378

Db 374 CAGATCCCTGGGCAAGCTGCGGCTTGAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 433

Qy 379 ACCTTGTCAGGGGAGCTGCTTCCCGGCACTGGAGCTTGAAGAGTGGAGGCTGGAGGCTCC 438

Db 434 ACCTTGTCAGGGGAGCTGCTTCCCGGCACTGGAGCTTGAAGAGTGGAGGCTGGAGGCTCC 493

Qy 439 TTCTATGACTGGGCGCTGACTGCTGAAGTGGCCACCAGCTGCTGCTGCTGCTGCTGCTGCT 498

Db 494 TTCTATGACTGGGCGCTGACTGCTGAAGTGGCCACCAGCTGCTGCTGCTGCTGCTGCTGCT 553

Qy 499 TTCCACACAGGCGCATCAAGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 558

Db 554 TTCCACACAGGCGCATCAAGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 613

Qy 559 TGGAAAGCGCGGAGCAAGCCCTGAGCGAGGATGCAAGTGTTCCTCCAGCTGTCAAGTTC 618

Db 614 TGGAAAGCGCGGAGCAAGCCCTGAGCGAGGATGCAAGTGTTCCTCCAGCTGTCAAGTTC 673

Qy 619 CTGCTCCGCTCAAAAGGAGAGACTTGTGCAAGTGTGCAAGGAGAGTCACTCCAGCTG 678

Db 674 CTGCTCCGCTCAAAAGGAGAGACTTGTGCAAGTGTGCAAGGAGAGTCACTCCAGCTG 733

Qy 679 CTGGGCTCTGGGACCCGCGGAGAAAGCCGGAAGACGACAGCCCTGCGCTGCTGCTGCTGCT 738

Db 734 CTGGGCTCTGGGACCCGCGGAGAAAGCCGGAAGACGACAGCCCTGCGCTGCTGCTGCTGCT 793

Qy 739 CTGGCTCTGGGATCCTGAGCTGCCCAACCCAGAGAGAGGATCCAGTCTGAAAGTGGC 798

Db 794 CTGGCTCTGGGATCCTGAGCTGCCCAACCCAGAGAGAGGATCCAGTCTGAAAGTGGC 853

Qy 799 CAGGAG----- 804

Db 854 CAGGAGCCAGAGAGGAGTCAAGTCCAGCCAGAGCCCAAGAGGCGTGGAGGTTCTTGAGCCC 913

Qy 805 CCAAGAGCCAGAGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 864

Db 914 CCAAGAGCCAGAGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 973

Qy 865 GTGGAGCTGAGCGGCGCGTGTCAAGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 924

Db 974 GTGGAGCTGAGCGGCGCGTGTCAAGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1033

Qy 925 GAGTGTGCCCCCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 984

Db 1034 GAGTGTGCCCCCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1093

Qy 985 CGGACCTTCTGCTTGAAGGCAAGTGGCCATGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1044

Db 1094 CGGACCTTCTGCTTGAAGGCAAGTGGCCATGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1153

Qy 1045 CTTGAGGCTCTGAGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1104

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QY 1165 CCGTTCGTCGCGGTGGGGAGGCTTAACTGACTCTGTTGGAGCTTCTGAATGAAAT 1224
Db 1274 CCGTTCGTCGCGGTGGGGAGGCTTAACTGACTCTGTTGGAGCTTCTGAATGAAAT 1333
QY 1225 AAGTGGGTTTCCCTGGAGGT 1246
Db 1334 AAGTGGGTTTCCCTGGAGGT 1355

RESULT 9
BD248275 1337 bp DNA linear PAT 17-JUL-2003
LOCUS BD248275
DEFINITION DNA encoding human apoptosis inhibitor, protein HIAP3.
ACCESSION BD248275.1 GI:33058045
VERSION JP 2002524039-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1337)
Deng, G., Lin, J. H. and Morner, M. J.
DNA encoding human apoptosis inhibitor, protein HIAP3
Patent: JP 2002524039-A 1 06-AUG-2002;
SCHERING AKTIEGENSCHAFT
OS Homo sapiens (human)
PN JP 2002524039-A/1
PD 06-AUG-2002
PR 23-JUL-1999 JP 2000563771
PI 31-JUL-1998 US 09/127928
PC 12N15/09, A61K31/7088, A61K35/76, A61K38/00, A61K45/00, A61K48/00,
PC A61P9/04, A61P9/10, A61P25/14, A61P25/28, A61P31/12, A61P35/00, PC
A61P37/02,
PC C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
, C12P21/02, C12Q1/68,
PC G01N33/15, G01N33/50, G01N33/53, G01N33/56, C12N15/00,
PC C12N5/00,
PC A61K37/02, A61K37/54
CC DNA encoding human apoptosis inhibitor, protein HIAP3 FH Key
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ORIGIN
Query Match 93.3%; Score 1162.4; DB 6; Length 1337;
Best Local Similarity 95.7%; Pred. No. 3.9e-203;
Matches 1227; Conservative 0; Mismatches 1; Indels 54; Gaps 1;

QY 19 GGCAGGCTGTGCTTATCCCTGCTGTCCGAGGTGGGCGCGGGGTGAGAGCTTCAG 78
Db 29 GGCAGGCTGTGCTTATCCCTGCTGTCCGAGGTGGGCGCGGGGTGAGAGCTTCAG 88
QY 79 AAGGCGCAGCTGGGCAATTTCTGAGATTGGCCATCAGCCCATTTCTGCTGCAAACTG 138
Db 89 AAGGCGCAGCTGGGCAATTTCTGAGATTGGCCATCAGCCCATTTCTGCTGCAAACTG 148
QY 139 GTCAAGACGAGTGTCCCTCCATGGAGACTTAAAGACAGTGCCTGAAGTGCCTGACCCGGA 198
Db 149 GTCAAGACGAGTGTCCCTCCATGGAGACTTAAAGACAGTGCCTGACCCGGA 208
QY 199 CCAAGCGGAGCACTGGGAGCGCGTGTATGTTCCACGAGAGCGCTGTGACCCCGC 258

Db 209 CCAAGCGGAGCACTGGGAGCGCGTGTATGTTCCACGAGAGCGCTGTGACCCCGC 268
QY 259 TTTCTGGGCGACCTGTGCTTAAGGCTTGGAACCTTGAGAGACCTGGGACCAACGTGGAATGG 318
Db 269 TTTCTGGGCGACCTGTGCTTAAGGCTTGGAACCTTGAGAGACCTGGGACCAACGTGGAATGG 328
QY 319 CAGATCCTGGGCGACGTCGGCCCTTGACAGAGAGGAAGAGAGAGGCGCGGGGCC 378
Db 329 CAGATCCTGGGCGACGTCGGCCCTTGACAGAGAGGAAGAGAGAGGCGCGGGGCC 388
QY 379 ACCTTGTCAAGGAGGCTGCTTCCCGGATGAGGCTTGAGAGATTGCGTTCGCTCC 438
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Db 449 TTTCAATGACGCGCGCTGACTGCTGAGGTGCACCCGAGCTGCTGCTGCTGCGGCTTC 508
QY 499 TTTCAACAGAGGCAATCAAGACAGAGTGAAGTGTCTTCTGCTATGAGGAGCTTGACAGC 558
Db 509 TTTCAACAGAGGCAATCAAGACAGAGTGAAGTGTCTTCTGCTATGAGGAGCTTGACAGC 568
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QY 1225 AAGTGGGTTTCCCTGGAGGT 1246

Db 1289 AAAGTGGGTTTCCCTGGAGGT 1310

RESULT 10
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LOCUS AR242238 1337 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6472172.
ACCESSION AR242238
VERSION AR242238.1 GI:27288060
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1337)
AUTHORS Deng, G., Lin, J.-H. and Morse, M.J.
TITLE DNA encoding a novel human inhibitor-of-apoptosis protein
JOURNAL Patent: US 6472172-A 1 29-OCT-2002;
Schering Aktieneseellschaft, Berlin;
DEX;

FEATURES
Source Location/Qualifiers
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ORIGIN
Query Match 93.3%; Score 1162.4; DB 6; Length 1337;
Best Local Similarity 95.7%; Pred. No. 3.9e-203;
Matches 1227; Conservative 0; Mismatches 1; Indels 54; Gaps 1;

QY 19 GGCAGGCTGTGCTATCCCTGCTGCTCCAGAGGTGGGCGGGGGTCAAGCTCCAG 78
Db 29 GGCAGGCTGTGCTATCCCTGCTGCTCCAGAGGTGGGCGGGGGTCAAGCTCCAG 88
QY 79 AAGGCGCAGCTGGGATATCTGAGATTGGCCATGAGCCCATTTCTGTGCAACCTG 138
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QY 679 CTGAGCTCTGGAGCCCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738
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QY 739 CTGCTCTGGAG 798
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QY 799 CAGAG----- 804
Db 809 CAGAGCCAG 868
QY 805 CAGAGCCAG 864
Db 869 CAGAGCCAG 928
QY 865 GTGCTCTGGAG 924
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Db 1109 CCGCCCTCTCTGCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1168
QY 1105 TGTGATCAGACAG 1164
Db 1169 TGTGATCAGACAG 1228
QY 1165 CCTTGTGCTGGAG 1224
Db 1229 CCTTGTGCTGGAG 1288
QY 1225 AAAGTGGGTTTCCCTGAGAGT 1246
Db 1289 AAAGTGGGTTTCCCTGAGAGT 1310

RESULT 11
AF301009 1168 bp mRNA linear PRI 05-DEC-2000
LOCUS AF301009
DEFINITION Homo sapiens inhibitor of apoptosis protein KIAA mRNA, complete cds.
ACCESSION AF301009
VERSION AF301009.1 GI:11545502
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1168)
AUTHORS Lin, J.-H., Deng, G., Huang, Q. and Morse, J.
TITLE A Novel member of the inhibitor of apoptosis protein family
JOURNAL Biochem. Biophys. Res. Commun. (2000) In press
AUTHORS Lin, J.-H., Deng, G. and Morse, J.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Cardiovascular Research, Berlex BioSciences Inc., 15049 San Pablo Ave., Richmond, CA 94804, USA
FEATURES
Source Location/Qualifiers
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RESULT 14
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DEFINITION Survivin-like polypeptide and its DNA.
ACCESSION BD185365.1 GI:31877565
VERSION BD185365.1
KEYWORDS JP 2002355062-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 840)
Tanaka, H. and Kaieda, I.
Survivin-like polypeptide and its DNA
TAKEDA CHEMICAL INDUSTRIES LTD
JP 2002355062-A/5
OS Homo sapiens (human)
PN JP 2002355062-A/5
PD 10-DEC-2002
PF 16-OCT-2001 JP 2001318533
PI HIROSHI TANAKA, ISAO KAIEDA
PC C12N15/09, A61K31/7088, A61K38/55, A61K39/395, A61K39/395, A61K48/
00, A61P35/00,
PC A61P43/00, A61P43/00, C07K44/82, C07K61/32, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, PC
G01N33/53,
PC G01N33/53, G01N33/566, G01N33/574, C12N15/00, C12N5/00, A61K37/64
CC Survivin-like polypeptide and its DNA
FH Key Location/Qualifiers
FT source 1..840
Location/Qualifiers
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ORIGIN
Query Match 67.3%; Score 838; DB 6; Length 840;
Best Local Similarity 99.8%; Pred. No. 1.2e-143;
Matches 838; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 160 ATGGAGCCTTAAAGACAGTGCCTGTCACCTGTGACCAAGCCGAGCCGACTGGGCA 219
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QY 220 GCCGGTATGTGTCCACGACGAGACCGCTGTGAGACCCCGCTTCTGCGGACGCTGTCTTA 279
Db 61 GCCGGTATGTGTCCACGACGAGACCGCTGTGAGACCCCGCTTCTGCGGACGCTGTCTTA 120

QY 280 GGCCTGACACCTGTCAGAGCTGTGGGACCAAGTGTGATGGGAGATCTGCGGACAGTGGG 339
Db 121 GGCCTGACACCTGTCAGAGCTGTGGGACCAAGTGTGATGGGAGATCTGCGGACAGTGGG 180

QY 340 CCCTGACAG 399
Db 181 CCCTGACAG 240

QY 400 TTCCCGGAG 459
Db 241 TTCCCGGAG 300

QY 460 GCTGAGGTGACACCCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
Db 301 GCTGAGGTGACACCCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

QY 520 AAGGTGAGGTGCTTCTTCTGCTATGAGGGGCTGACAGAGCTGGAAGCGCGGGAGAGAGAG 579

Db 361 AAGGTGAGGTCTTCTTCTGCTATGAGGGGCTGTGACAGCTGGAAGCGCGGGAGAGAGAG 420

QY 580 TGGACGAGAGATGCGCAAGTGGTTCCAGAGCTGTGAGTTCCTGCTCCGGTCAAAAGAGA 639
Db 421 TGGACGAGAGATGCGCAAGTGGTTCCAGAGCTGTGAGTTCCTGCTCCGGTCAAAAGAGA 480

QY 640 GACTTTGTGCAACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTCTGCGGACCGGTG 699
Db 481 GACTTTGTGCAACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTCTGCGGACCGGTG 540

QY 700 GAAGAACCGGAAGACGAGCGCCCTGTGGCCCTCCCTGCTGCTGCTGCTGCTGCTGAG 759
Db 541 GAAGAACCGGAAGACGAGCGCCCTGTGGCCCTCCCTGCTGCTGCTGCTGCTGCTGAG 600

QY 760 CTGCCACACCCGAGAGAGAGTCACTGGAAGTCCAGAGCCAGAGCCAGAGAT 819
Db 601 CTGCCACACCCGAGAGAGAGTCACTGGAAGTCCAGAGCCAGAGCCAGAGAT 660

QY 820 GTGAGGCGGAGCTGCGCGCGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
Db 661 GTGAGGCGGAGCTGCGCGCGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 880 GCCGTGTCAATCGTCTTTGTCGCGTGGCGGCACTGTGTGTGTGAGTGTGCCCCGGC 939
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QY 940 CTGACGCTGTGCCCCCATCTGACAGAGCCCCCGTCGACGCGCGCTGCGACCTTCTGTGC 999
Db 781 CTGACGCTGTGCCCCCATCTGACAGAGCCCCCGTCGACGCGCGCTGCGACCTTCTGTGC 840

RESULT 15
AY517497
LOCUS AY517497 1021 bp mRNA linear PRI 03-FEB-2004
DEFINITION Homo sapiens baculoviral IAP repeat-containing 7 (BIRC7) mRNA,
complete cds, alternatively spliced.
ACCESSION AY517497
VERSION AY517497.1 GI:41387694
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1021)
Li, H., Ke, R., Wang, C., Zhou, G., Shen, C., Lin, L. and Yang, S.
Direct Submission
Submitted (03-JAN-2004) Guangzhou Pulengen Co., Ltd., 5/F.,
Guangzhou Entrepreneur Park for Overseas Chinese Scholars, 11
Baoshi Rd., GENDU, Guangzhou, Guangdong 510730, China

FEATURES
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Location/Qualifiers
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GRGPGC"

ORIGIN

Query Match 52.4%; Score 653.4; DB 8; Length 1021;
Best Local Similarity 82.5%; Pred. No. 8.4e-110;
Matches 842; Conservative 0; Mismatches 1; Indels 178; Gaps 1;

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DB 61 GCCGGTATGATGGTCCACAGCAGAGGCGCTGTGGACCCCGCTTCTTGGGCAAGCCCTGTCTTA 120
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QY 340 CCCCTGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
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Job time : 6627 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 21:43:05 ; Search time 5614 Seconds
(without alignments)
10384.165 Million cell updates/sec

Title: US-09-762-577B-11

Perfect score: 1246
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	762	61.2	891	6	CD051153 AGENCOURT
2	721.8	57.9	929	5	BQ892691 AGENCOURT
3	718.4	57.7	843	11	DQ053047 Homo sapi
4	715	57.4	884	5	BUI95879 AGENCOURT
5	715	57.4	924	5	BQ682827 AGENCOURT
6	712.4	57.2	982	5	BQ682897 AGENCOURT
7	711.2	57.1	824	2	BG770578 AGENCOURT
8	709.8	57.0	830	2	BG762467 AGENCOURT
9	709.8	57.0	912	5	BQ682378 AGENCOURT
10	702	56.3	870	5	BQ877438 AGENCOURT
11	694.4	55.7	945	5	BUI80020 AGENCOURT
12	692.8	55.6	842	2	BG770473 AGENCOURT
13	690.8	55.4	958	5	BUI88703 AGENCOURT
14	686.8	55.1	919	5	BQ877652 AGENCOURT
15	675.4	54.2	920	5	BQ676590 AGENCOURT
16	674.8	54.0	956	2	BUI72109 AGENCOURT
17	673.2	54.0	877	2	BG770075 AGENCOURT
18	666	53.5	902	5	BUI83453 AGENCOURT
19	664.8	53.4	808	2	BG761924 AGENCOURT
20	654.8	52.6	740	2	BG768992 AGENCOURT
21	651	52.2	797	2	BG766472 AGENCOURT
22	645.8	51.8	994	2	BF690534 AGENCOURT

23	644	51.7	655	2	BG760550
24	638.6	51.3	849	2	BG760865
25	636	51.0	741	2	BG763960
26	625.8	50.2	843	2	BG766949
27	621	49.8	621	6	CD673774
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29	612.8	49.2	968	5	BQ679311
30	611	49.0	652	2	BG763730
31	602.4	48.3	632	5	BUI742147
32	599.8	48.1	616	2	BG767481
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36	580.2	46.6	956	5	BUI68025
37	560.6	45.0	579	6	CD673799
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39	553.8	44.4	720	6	CA306197
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41	549.2	44.1	646	2	BG769461
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44	510.8	41.0	872	5	BQ878898
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ALIGNMENTS

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DEFINITION CD051153
ACCESSION CD051153.1 GI:30488777
VERSION
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 891)
NIH-MGC http://mgc.ncl.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

Tissue Procurement: Dr. Jamie Thompson, University of WI
CDNA Library Preparation: Gina Zaetrow-Hayes
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: NDKM35 row: d column: 07
High quality sequence start: 18
High quality sequence stop: 718.

FEATURES

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LIBR PROVIDER - Bradfield"

ORIGIN

Query Match 61.2%; Score 762; DB 6; Length 891;
Best Local Similarity 96.8%; Pred. No. 5.8e-163;
Matches 788; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

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 DB 123 GTCAAGCCAGTGTTCCTCCATGAGACCTTAAGA CAGTGCACAGTGCCTTGCACCCGTGA 252
 QY 199 CCAAGCCGAGGCACTGGGCAAGCCGATGATGATCCCAAGAGAGCGCTGGACCCCGC 258
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 5', mRNA sequence.
 ACCESSION B0892691
 VERSION B0892691.1 GI:22284705
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Buzayvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 929)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE
 JOURNAL
 COMMENT
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNC2325 row: a column: 17
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 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN
 Query Match 57.9%; Score 721.8; DB 5; Length 929;
 Beet Local Similarity 99.6%; Pred. No. 8,7e-154;
 Matches 734; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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OY		940	CTGCAGCTGTGCCCATCTGACAGCCCGGCTGCCAGCCGCGGTGCGCACTTCTGTCC	999
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VERSION		BUI95879.1 GI:22709863		
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		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
		Hominidae; Homo.		
REFERENCE		1 (bases 1 to 884)		
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/.		
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL		Unpublished (1999)		
COMMENT		Contact: Robert Strausberg, Ph.D. Email: rgabbs@email.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LMNL) DNA Sequencing by: Agencourt Bioscience Corporation		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLI at: <http://image.llnl.gov>

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High quality sequence stop: 658.

FEATURES

Location/Qualifiers

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ORIGIN

Query Match

Best Local Similarity 57.4%; Score 715; DB 5; Length 884;

Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

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RESULT 5

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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B0682827
B0682827.1 GI:21795506
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 924)
NIH-MGC <http://mgi.mcl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/DP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
<http://image.llnl.gov>
Plate: LNCM2499 row: 0 column: 05
High quality sequence stop: 673.

FEATURES

Location/Qualifiers

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/clone="IMAGE:6294748"
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/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity 57.4%; Score 715; DB 5; Length 924;

Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 97 TTCTGAGATTGGCCATGAGCCCATTTCTGTCGCAAACTGGTCAGAGCCATGTTCCC 156
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Db 61 TCCATGGAGCCTTAAGACAGTCCCAAGTGCCTGACCGTGGACACAGCCGACCACTAG 120
QY 217 GCAAGCCGGTATGGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276
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QY 277 CTAGGCTTGAACACCTGACAGAGCTTGGAGCAACGTGATGGAGATCTTGGGCCAGCTG 336
Db 181 CTAGGCTTGAACACCTGACAGAGCTTGGAGCAACGTGATGGAGATCTTGGGCCAGCTG 240
QY 337 CGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396

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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF

CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNCM715 row: k column: 02
High quality sequence stop: 799.
Location/Qualifiers

FEATURES

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into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library." "

ORIGIN

Query Match 57.1%; Score 711.2; DB 2; Length 824;
Best Local Similarity 97.0%; Pred. No. 2.2e-151;
Matches 778; Conservative 0; Mismatches 18; Indels 6; Gaps 5;

6 CGAGCTGTCGCGGCGAGGCTGCTATCCCTGCTGCTCCCGAGGTTGGCCCGCGGGG 65
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78 TCAGAGCTCCAGAGGGGCGAGCTGGGCAATTCAGATGGCCATCAGCCCATTTTC 137
126 TGCTGCAAACTGTGTCAGAGCCAGTGTCCCTTCATGGAGCACTAAAGACATGCCAAGTG 185
138 TGCTGCAAACTGTGTCAGAGCCAGTGTCCCTTCATGGAGCACTAAAGACATGCCAAGTG 197
186 CCGTCACCGTCGACCAAGCCGAGCTGAGGCAAGCGGTGATGGTCCACGACAGAGACG 245
198 CCGTCACCGTCGACCAAGCCGAGCTGAGGCAAGCGGTGATGGTCCACGACAGAGACG 257
246 CTGTGAGACCCGCTCTCTGGGAGAGCCCTTCTTAAAGCTTGGACACCTTCAGAGCTTGGGA 305
258 CTGTGAGACCCGCTCTCTGGGAGAGCCCTTCTTAAAGCTTGGACACCTTCAGAGCTTGGGA 317
306 CCACGTGATGAGGAGATCTGAGGCAAGCTGAGGCGCCCTTCAGACAGAGAGAGAGAGAGA 365
318 CCACGTGATGAGGAGATCTGAGGCAAGCTGAGGCGCCCTTCAGACAGAGAGAGAGAGAGA 377
366 GGGGCGCGGGGCGACATCTGTCCAGGGGGCGCTGCTTCCCGGCAATGGGCTCTGAGAGATT 425
378 GGGGCGCGGGGCGACATCTGTCCAGGGGGCGCTGCTTCCCGGCAATGGGCTCTGAGAGATT 437
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QY 546 GGGCTTCAGAGAGTGGAAAGCGCGGGAGACACCCCTTGAACGAGCATGCCAATGTGTTCCC 605
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VERSION BG762467.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 830)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNCM714 row: f column: 03
High quality sequence stop: 802.
Location/Qualifiers

FEATURES

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/clone_lib="NIH MGC 49"
/note="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2:
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library." "

ORIGIN

Query Match 57.0%; Score 709.8; DB 2; Length 830;
Best Local Similarity 95.0%; Pred. No. 4.7e-151;
Matches 765; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

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 DB 28 GGCAGGCTGTGCTTATCCCTGCTGTGCTCCAG-GGTGGGCGCGGGGTCAAGAGCTCCAG 86
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 QY 139 GTCAAGAGCAGTGTTCCTCCATGGGAGCCTAAAGACAGTGCAGATGCTGCTGACCGTGA 198
 DB 147 GTCAAGAGCAGTGTTCCTCCATGGGAGCCTAAAGACAGTGCAGATGCTGCTGACCGTGA 206
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 DB 207 CCACAGCCGAGCAGCTGGGAGCGGTGATGATGATCCACGACAGAGCGCTGTGAGACCCGCG 266
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 DB 267 TCTTGTGGGAGAGCCTGTGCTTGGGCTGAGACCTGTGAGAGCTGTGAGAGCTGTGAGAG 326
 QY 319 CAGATCTGGGAGAGCCTGTGCTTGGGCTGAGACCTGTGAGAGCTGTGAGAGCTGTGAGAG 378
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 QY 379 ACCTGTGTCAGAGGGGCTGTGCTTGGGCTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 438
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 QY 499 TTCCACAGGCGCATCAAGAGCAAGGTGAGTCTTCTGCTATGAGGGGCTGTGAGAGCTGTGAGAG 558
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 QY 559 TGAAGGCGGGGAG 618
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 DB 627 CTGCTCGGCTCAAAAG 686
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RESULT 9
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 ACCESSION AGENCOURT 8185884 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6263255
 VERSION B0682378
 KEYWORDS B0682378.1 GI:21795057
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo
 1 (bases 1 to 912)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9abs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2426 row: n column: 24
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 /lab_host="DH10B (phage-resistant)"
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 /note="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: This is a
 NIH_MGC Library."

ORIGIN
 Query Match 57.0%; Score 709.8; DB 5; Length 912;
 Best Local Similarity 99.6%; Pred. No. 4.8e-151;
 Matches 711; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 97 TTCTGAGATTGGCCATCAGCCCATTTCTGCTGCAAACTGTGTCAGAGCAGTGTCCC 156
 DB 1 TTCTGAGATTGGCCATCAGCCCATTTCTGCTGCAAACTGTGTCAGAGCAGTGTCCC 60
 QY 157 TCCATGGAGCTTAAAGACAGTGCAGAGCTGTGACCCGTGACAGAGCCGAGCCACTGG 216
 DB 61 TCCATGGAGCTTAAAGACAGTGCAGAGCTGTGACCCGTGACAGAGCCGAGCCACTGG 120
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 DB 121 GCAGCCGGTGAATGCTCCAGAGAGCGGTGTGAGACCCGCTCTGAGGCAAGCCCTGTC 180
 QY 277 CTAGGCTGGACACCTGAGAGCTGGAGACCACTGATGGAGATCCCTGGGCAAGCTG 336
 DB 181 CTAGGCTGGACACCTGAGAGCTGGAGACCACTGATGGAGATCCCTGGGCAAGCTG 240
 QY 337 CGGCCCCCTGACAG 396
 DB 241 CGGCCCCCTGACAG 300
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 QY 457 ACTGCTGAGGTGACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 516
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Db	601	TGGAAAGAACCGGAAGACGCAAGCCCTCTGTGGCCCTCCGTCCTCCTCTGAGTACCT	660
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LOCUS			
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KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
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AUTHORS	1 (bases 1 to 870)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cga@bhs-remail.nih.gov Tissue Procurement: DCDT/DTF CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LINC2331 row: e column: 07 High quality sequence stop: 380. Location/Qualifiers 1. .870 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6090222" /tissue_type="melanotic melanoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."		
FEATURES			
source			
Query Match	56.3%; Score 702; DB 5; Length 870;		
Best Local Similarity	99.7%; Pred. No. 2.9e-149;		
Matches 713; Conservative	0; Mismatches 1; Indels 1; Gaps 1;		
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Qy	157	TCCATGGGACCTTAAGACAGTGCACAGTGCCTTSCACCGTGGACACAGCCGACCACTGG	216
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Qy	217	GCAAGCGGTGATGTCCTCCACGACGAGACGCTGTGACCCGCTCTCTGAGGACCCCTGTC	276
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Qy	27	CTAGAGCCTGGACACCTTGCAGAGCCTTGAGACCAACGTGATGAGCAGATCTTGAGGCACGCTG	336
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Qy	337	CGAGCCCTCTGACAGAGAGGAAAGAGAGAGAGGCGCCGAGGCGCACCTTGTCCAGAGGAGCCT	399
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Qy	457	ACTGCTGAGGTGCAACCCGAGCTGTGAGCTGCGCGGCTTCTTCCACACAGGCCATACG	516
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Qy	517	GACAAAGTGAAGTGTCTTCTTCTGCTATGAGGAGCCTTGACAGCTGGAAGCGCGGAGCGAC	576
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Db	601	TGGGAAGAACCGGAGAGACGACAGCCCTGATGGCCCCCTCCGCTCTGAGGTATACC	660
Qy	756	TGAGCTGCCACACCCAGAGAGAGGTCCAGTGTGAAAGTGCCCGACGAGCCAGCA	810
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BUI180020.1 GI:22694004			
EST.			
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Homo sapiens			
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
1 (bases 1 to 945)			
NIH-MGC http://mgc.nci.nih.gov/			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: rs9aps-r@mail.nih.gov			
Tissue Procurement: DCTD/DTF			
CDNA Library Preparation: Rubin Laboratory			
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LNL at:			
http://image.lnl.gov			
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FEATURES

source

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 DB 667 CTGGGCTCTGGGACCCGCTGGGAGAAACCGGAAACGAGCCCTGTGTGCCCCCTCCGTC 722
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 DB 723 CCTGCTCTGGGTAACCTGAGCTGCCACACCCGAGAGAGAGGTCCAGTCTGAAGTGC 780

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 VERSION BU188703.1 GI:22702687
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 958)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LILNL at:
 http://image.jnl.gov

plate: LHC2347 row: C column: 07
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 Location/Qualifiers

FEATURES

source

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 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 55.4%; Score 690.8; DB 5; Length 958;
 Best Local Similarity 98.5%; Pred. No. 18-146;
 Matches 719; Conservative 0; Mismatches 7; Indels 4; Gaps 2;

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 DB 64 GGCAGGCTGTGCTATCCCTGCTGCTCCCAAGGTGTGGCCCGGGGTATAGAGCTCCAG 123
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 DB 124 AAGGGCAGCTGGGATATTTCTGAGATTGGCCATGAGCCCATTTCTGCTCAACCTG 183
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 DB 304 TCTTGGGCTAGCCTGTGTCTTGAAGCTTGAACCTTGAGACCTTGAGACCACTGTGATGG 363
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 QY 379 ACCTTGTCCAGGGGCTCTGCTTCCCGCATGTGGCTCTGAGAGTTGCTGTGGCTTCC 438
 DB 424 ACCTTGTCCAGGGGCTCTGCTTCCCGCATGTGGCTCTGAGAGTTGCTGTGGCTTCC 483
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 DB 664 CTGCTCCGCTCAAAAGGAAAGAGACTTGTCTCAGAGTGTGAGAGACTCACTCCCACTG 723
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RESULT 14
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 LOCUS AGENCOURT_8095636 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6087869
 DEFINITION 5', mRNA sequence.
 ACCESSION BO877652
 VERSION BO877652.1 GI:22269660
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 919)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9abds-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LICM2325 row: C column: 06
 High quality sequence stop: 604.
 Location/Qualifiers

FEATURES

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 /clone_id="NIH MGC 112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match

Best Local Similarity 99.2%; Score 686.8; DB 5; Length 919;
 Matches 710; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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QY 157 TCCATGGGACCTTAAAGACAGTGCACAGTGCCTGCACCTGTGACACACAGCCGACCTG 216
DB 61 TCCATGGGACCTTAAAGACAGTGCCTGCACCTGTGACACACAGCCGACCTG 120
QY 217 GCAGCCGGTATGGTCCCAAGAGAGCGCTGTGACCCCGCTCTCTGGGACGCTGTC 276
DB 121 GCAGCCGGTATGGTCCCAAGAGAGCGCTGTGACCCCGCTCTCTGGGACGCTGTC 180
QY 277 CTAGGCTTGGACACTGTCAGAGGCTTGGACCAAGTGGATGGGACATCTGGGACAGCTG 336
DB 181 CTAGGCTTGGACACTGTCAGAGGCTTGGACCAAGTGGATGGGACATCTGGGACAGCTG 240
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DB 301 GCCTTCCCGGACATGGGCTCTGAGAGAGTGGTCTGGGCTCTTCTATGACTGGCGGCTG 360
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DB 361 ACTGCTGAGGTGTCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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DB 541 AAGACTTTGTCCACAGTGTGACAGAGACTCACTCCCAAGTGTGAGGCTCTGAGACCCC 600

QY 696 GTGGGAAGAACCGGAAGAGAGCAGCCCTGTGGGCCCTCCGTCCTGCTGCTGCTGCTGCTG 755

DB 601 GTGGGAAGAACCGGAAGAGAGCAGCCCTGTGGGCCCTCCGTCCTGCTGCTGCTGCTGCTG 660

QY 756 TGAGTGGCCCAACCCAGAGAGAGAGTTCAGTCTGAAAGTGGCCAGAGAGCCAGAG 811

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RESULT 15

LOCUS

BQ676590 920 bp mRNA linear EST 15-JUN-2002
 AGENCOURT 8194873 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6258969

DEFINITION

5', mRNA sequence.

ACCESSION

BQ676590 GI:21789269

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9abds-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LICM2415 row: 1 column: 10
 High quality sequence stop: 609.
 Location/Qualifiers

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6258969"
 /issue_type="melanotic melanoma, cell line"
 /lab_host="NIH MGC 112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match

Best Local Similarity 96.9%; Score 675.4; DB 5; Length 920;
 Matches 688; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 157 TCCATGGGACCTTAAAGACAGTGCACAGTGCCTGCACCTGTGACACACAGCCGACCACTGG 216
DB 61 TCCATGGGACCTTAAAGACAGTGCACAGTGCCTGTGACACACAGCCGACCACTGG 120
QY 217 GCAGCCGGTATGGTCCCAAGAGAGCGCTGTGACCCCGCTCTCTGGGACGCTGTC 276
DB 121 GCAGCCGGTATGGTCCCAAGAGAGCGCTGTGACCCCGCTCTCTGGGACGCTGTC 180

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 23:16:46 ; Search time 1160 Seconds
(without alignments)
8882.453 Million cell updates/sec

Title: US-09-762-577B-11
Perfect score: 1246
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1228	98.6	1260	6 US-10-188-646-4	Sequence 4, Appl
2	1228	98.6	1260	8 US-10-807-897-28	Sequence 26, Appl
3	1228	98.6	1376	5 US-10-244-586-1	Sequence 1, Appl
4	1164	93.4	1322	8 US-10-807-897-26	Sequence 26, Appl
5	1162.4	93.3	1337	5 US-10-235-026-1	Sequence 1, Appl
6	1159.4	93.0	1363	8 US-10-839-882-37	Sequence 37, Appl
7	1021.4	82.0	1168	6 US-10-188-646-12	Sequence 12, Appl
8	843	67.7	843	5 US-10-244-586-2	Sequence 2, Appl
9	729.8	58.6	3782	9 US-10-450-763-27357	Sequence 27357, A
10	675	54.2	769	6 US-10-203-708-32	Sequence 22, Appl
11	640.6	51.4	858	6 US-10-723-860-8265	Sequence 8265, A
12	590	47.4	676	8 US-10-723-860-4448	Sequence 4448, A
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14	492.4	39.5	4810	6 US-10-188-646-11	Sequence 11, Appl
15	449	36.0	449	8 US-10-723-860-4697	Sequence 4697, A
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17	433.6	34.8	614	9 US-10-450-763-27354	Sequence 27354, A
18	317.8	25.5	444	9 US-10-450-763-27355	Sequence 27355, A
19	301.4	24.2	399	9 US-10-983-495-1	Sequence 1, Appl
20	224	18.0	226	7 US-10-641-643-334	Sequence 334, App
21	160.4	12.9	404	6 US-10-779-543-12365	Sequence 12365, A
22	135	10.8	200	6 US-10-305-720-216	Sequence 216, App
23	135	10.8	200	7 US-10-641-643-387	Sequence 387, App

24	97	7.8	2450	3 US-09-201-936-39	Sequence 39, Appl
25	97	7.8	2474	7 US-10-636-065-226	Sequence 226, App
26	97	7.8	2474	7 US-10-600-272-39	Sequence 39, Appl
27	97	7.8	2673	8 US-10-482-952-2	Sequence 2, Appl
28	97	7.8	2676	3 US-09-974-592-11	Sequence 11, Appl
29	91.8	7.4	3773	5 US-10-041-859-1	Sequence 1, Appl
30	86.6	7.0	2862	6 US-10-232-286-13	Sequence 13, Appl
31	86.6	7.0	2862	8 US-10-934-717-13	Sequence 13, Appl
32	86.6	7.0	3151	3 US-09-974-592-13	Sequence 13, Appl
33	86.6	7.0	3151	8 US-10-482-952-4	Sequence 4, Appl
34	85	6.8	2416	3 US-09-201-936-41	Sequence 41, Appl
35	85	6.8	2416	7 US-10-636-065-228	Sequence 228, App
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37	80.8	6.5	1435	2 US-08-464-588-1	Sequence 1, Appl
38	80.8	6.5	1435	5 US-10-323-643-1	Sequence 1, Appl
39	80.8	6.5	2531	5 US-10-207-655-199	Sequence 199, App
40	80.8	6.5	2531	9 US-10-485-225-64	Sequence 64, Appl
41	80.8	6.5	2531	9 US-10-287-436A-670	Sequence 670, App
42	80.8	6.5	2589	6 US-10-232-286-1	Sequence 1, Appl
43	80.8	6.5	2589	7 US-10-730-476A-42	Sequence 42, Appl
44	80.8	6.5	2589	7 US-10-730-476A-43	Sequence 43, Appl
45	80.8	6.5	2589	8 US-10-934-717-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-188-646-4
; Sequence 4, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1016)
US-10-188-646-4

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			Indels	0
			Gaps	0
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QY	79	AAGGCGCAGTGGGCAATTTGAGATTGGCCATCAGCCCACTTTCTGCTCAAACTG	138	
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QY	139	GTCAGAGCAGTGTTCCTCCATGGAGCACTAAAGACAGTGGCCAGGCTGCAGCGTGA	198	
DB	153	GTCAGAGCAGTGTTCCTCCATGGAGCACTAAAGACAGTGGCCAGGCTGCAGCGTGA	212	
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QY	259	TCTTGTGGGAGCCCTCTCTAGGCTTCGACACTGTGAGAGCTTCGAGCAACGATGG	318	
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RESULT 4

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US-10-807-897-26
; Sequence 26, Application US/10807897
; Publication No. US2004019261A1
; GENERAL INFORMATION:
; APPLICANT: Xiang, Hong
; APPLICANT: Zhou, He
; APPLICANT: Reisfeld, Ralph A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; FILE REFERENCE: TSPRI-874.1
; CURRENT APPLICATION NUMBER: US/10/807,897
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,009
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1322
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1070)
US-10-807-897-26

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Query Match 93.4%; Score 1164; DB 8; Length 1322;
 Best Local Similarity 95.8%; Pred. No. 6.1e-306;
 Matches 1228; Conservative 0; Mismatches 0; Indels 54; Gaps 1;

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Db 93 AAGGGCAGCTGGGCAATTTCTGAGATTGGCCATTCAGCCCCCATTTCTGTGCAAACTGG 152
QY 139 GTCAGAGCCAGTGTTCCTCCATGAGACCTAAAGACAGTGCACAGTGCCTGACCGTGG 198
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QY 199 CCAAGCCGAGCCACATGGGAGCCGGTGAATGTCCTCCACCGAGAGCGCTGTGACCCCGC 258
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QY 319 CAGATCTCTGGGAGCTGTGGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
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QY 739 CTGCTCTGGGATACCTGAGCTGACACACCCAGAGAGAGAGAGAGAGAGAGAGAGAG 798
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QY 799 CAGAG----- 804
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RESULT 5

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US-10-235-026-1
; Sequence 1, Application US/10235026
; Publication No. US20030082725A1
; GENERAL INFORMATION:
; APPLICANT: Deng, Gang
; APPLICANT: Lin, Jiling-Huey
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: DNA Encoding a No. US20030082725a1e1 Human Inhibitor-of-Apoptosis
; FILE REFERENCE: 50972AUSD1
; CURRENT APPLICATION NUMBER: US/10/235,026
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 09/127,928
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)...(1066)
; OTHER INFORMATION:

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US-10-2335-026-1

Query Match	93.3%	Score 1162.4;	DB 5;	Length 1337;
Best Local Similarity	95.7%;	Pred. No. 1.6e-305;		
Matches 1227; Conservative	0;	Mismatches 1;	Indels 54;	Gaps 1;

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QY	319	CAGATCTCTGGGCCACGTGGCCGCCCTCTGACAGAGAGAAAGAGAGAGAGGGCGCCGGGGCC	378
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QY	379	ACCTTGTTCAGAGGGGGGCTGCTCTTCCCGGCAGTGGGCTCTGAGAGATTGCGTCTGGACCTCC	438
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QY	499	TTTCCACACAGGCCCATCAGAGCAAGGTAGGTCTTTCTTGTCTATATGGGGGCTTGCACAGC	558
Db	509	TTTCCACACAGGCCCATCAGAGCAAGGTAGGTCTTTCTTGTCTATATGGGGGCTTGCACAGC	568
QY	559	TGGAAAGCCGGGGAGCGACCCCTGTGACGGAGCATCCAAAGTGTTCCTCCAGCTGTCAATTTC	618
Db	569	TGGAAAGCCGGGGAGCGACCCCTGTGACGGAGCATCCAAAGTGTTCCTCCAGCTGTCAATTTC	628
QY	619	CTGTCTCCGGTCTAAAGAGAGAGACTTTGTCTCAAGTGTGCAGAGACTCACTTCCAGCTG	678
Db	629	CTGTCTCCGGTCTAAAGAGAGAGACTTTGTCTCAAGTGTGCAGAGACTCACTTCCAGCTG	688
QY	679	CTGGGGCTCTGGGAGCCCGTGGGAGAAACCGGAAACGCAAGCCCTGTGGGCCCTTCCGTTC	738
Db	689	CTGGGGCTCTGGGAGCCCGTGGGAGAAACCGGAAACGCAAGCCCTGTGGGCCCTTCCGTTC	748
QY	739	CTTGCCCTTCTGGGTACCCCTGAGCTGCCACACCCAGAGAGAGATCTCAGTCTGAAGTGGC	798
Db	749	CTTGCCCTTCTGGGTACCCCTGAGCTGCCACACCCAGAGAGAGATCTCAGTCTGAAGTGGC	808
QY	799	CAGAGG-----	804
Db	809	CAGAGGCCAGAGAGGGAGTCAGTCCAGCCGAGGCCACAGAGGGCGTGTGGGTCTTTAGAGCC	868
QY	805	CCAAGGACCAAGGAGTGTGGAGGCGCAGCTGCGCGGCTGCAGAGAGAGAGAGAGCTGGCAG	864
Db	869	CCAAGGACCAAGGAGTGTGGAGGCGCAGCTGCGCGGCTGCAGAGAGAGAGAGAGAGCTGGCAG	928
QY	865	GTTGTGCTTGAACCGCGCCGTGTCCATGTCCTTTGTGCCGTGGCCACCTGTGTGTGTCT	924
Db	929	GTTGTGCTTGAACCGCGCCGTGTCCATGTCCTTTGTGCCGTGGCCACCTGTGTGTGTCT	988
QY	925	GAGGTGTGCCCCCGGCGCTGACAGCTGTGGCCCATCTGACAGAGGCCCGCGTCCGAGCGGGGTG	984
Db	989	GAGGTGTGCCCCCGGCGCTGACAGCTGTGGCCCATCTGACAGAGGCCCGCGTCCGAGCGGGGTG	1048

QY	985	CGACCTTCCCTGCTCTGAGGCGCAAGTGCATGCGCCGCGCAGAGTGGCGCTC	1044
Db	1049	CGACCTTCCCTGCTCTGAGGCGCAAGTGCATGCGCCGCGCAGAGTGGCGCTC	1108
QY	1045	CTGCGCCCTCTCTGCGCTGTTCTGAGACTGTCTTGCGGCTCTGAGAGATGGCAGACTGG	1104
Db	1109	CTGCGCCCTCTCTGCGCCCTGTTCTGAGACTGTCTTGCGGCTCTGAGAGATGGCAGACTGG	1168
QY	1105	TGTCATTCAGCACTGACCAAGCCCTGATTTCCCGGACCAACCGCCAGAGGTGAGAGAGAG	1164
Db	1169	TGTCATTCAGCACTGACCAAGCCCTGATTTCCCGGACCAACCGCCAGAGGTGAGAGAGAG	1228
QY	1165	CCCTTGCTTGGCGTGGGGGATGGCTTAACTGTACCTGTTTGATGCTTCTGAATTAAGAAAT	1224
Db	1229	CCCTTGCTTGGCGTGGGGGATGGCTTAACTGTACCTGTTTGATGCTTCTGAATTAAGAAAT	1288
QY	1225	AAAGTGGGTTTTCCCTGAGAGT	1246
Db	1289	AAAGTGGGTTTTCCCTGAGAGT	1310

```

RESULT 6
US-10-839-882-37
; Sequence 37, Application US/10839882
; Publication No. US20040203106A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: LAL, Preeti
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: JUNGUNG, Yang
; APPLICANT: SHH, Leo L.
; TITLE OF INVENTION: PROLIFERATION AND APOPTOSIS RELATED PROTEINS
; FILE REFERENCE: PE-0619 PCT
; CURRENT APPLICATION NUMBER: US/10/839,882
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US/09/807,452
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/175,737; unassigned; 60/118,559; 09/249,740; unassigned; 60/154,336
; PRIOR FILING DATE: 1998-10-20; 1998-10-20; 1999-02-04; 1999-04-11; 1999-04-11; 1999-04-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 37
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1520835CBI
; US-10-839-882-37

```

Query Match	95.0%;	Score 1159.4;	DB 8;	Length 1363;
Best Local Similarity	93.7%;	Pred. No. 1, 1e-304;		
Matches 1222;	Conservative	0;	Mismatches 1;	Indels 54;
Gaps				1;
QY	19	GGCAGCCTGTGTGCTATCCCTGTGTCGCCAAGGTGGGCCCGGGGGGTGAGAGCTCCAG	78	
Db	74	GGAGGGCTGTGTGCTATCCCTGTGTCGCCAAGGTGGGCCCGGGGGGTGAGAGCTCCAG	133	
QY	79	AAGGGCAGCTGGGCGATATTGTAGATWTGGCCATCAGCCCCATTTCCTGCAAACTGG	138	
Db	134	AAGGGCAGCTGGGCGATATTGTAGATWTGGCCATCAGCCCCATTTCCTGCAAACTGG	193	
QY	139	GTCAGGCCAGTGTTCCTTCATGGGACCTAAAGACAGTGCACGCTGCAACCGTGA	198	

Db	601	CTGCCCA	CACCAGGAGAGAGGTCCAGTCTGAAGTGCCTCAGAGACCAGAGGGGTCACT	660
Qy	805	-----	-----CCAGAGCCAGGAGATGTGGAG	825
Db	661	CCAGCCGAGG	CCCAAGAGGCGTGTGTGGTTCTTGGAGCCCCCAGGAGGCCAGGGAATGTGAG	720
Qy	826	GCGCAGCTGG	CGGCGGCTGCAGAGAGAGACGTGTCAAGGTGTGTCTGACACCGGCGCTGG	885
Db	721	GCGCAGCTGG	CGGCGGCTGCAGAGAGAGACGTGTCAAGGTGTGTCTGACACCGGCGCTGG	780
Qy	886	TCCATCTGCTT	TGTGTCCCGTCCGACCACTGAGTCTGTGATGTGTGCCCGGCGCTGGAG	945
Db	781	TCCATCTGCTT	TGTGTCCCGTCCGACCACTGAGTCTGTGATGTGTGCCCGGCGCTGGAG	840
Qy	946	CTGTGCCCCAT	CTGTGAGAGCCCCCGCTCCGACGCCGCGTGCACACTTCTCTGTCTAGGCC	1005
Db	841	CTGTGCCCCAT	CTGTGAGAGCCCCCGCTCCGACGCCGCGTGCACACTTCTCTGTCTAGGCC	900
Qy	1006	AGCTGCCATAG	CGGCGGCTGCAGAGTGGGTGTGAGAGTGGGCTCCCTGCGCCCTCTCTGTCTGTTC	1065
Db	901	AGGTGCCATAG	CGGCGGCTGCAGAGTGGGTGTGAGAGTGGGCTCCCTGCGCCCTCTCTGTCTGTTC	960
Qy	1066	TGCACTGATGT	CTGTGGGCGCTGTGAGAGATGGCAGAGCTGTGTGTCAATCCAGACTGACCCAG	1125
Db	961	TGCACTGATGT	CTGTGGGCGCTGTGAGAGATGGCAGAGCTGTGTGTCAATCCAGACTGACCCAG	1020
Qy	1126	CCCTGATTTCC	CCGACCAACCGCCGACAGGGTGGAGAGAGAGGCCCTTGTGCGGTGGGGGAT	1185
Db	1021	CCCTGATTTCC	CCGACCAACCGCCGACAGGGTGGAGAGAGAGGCCCTTGTGCGGTGGGGGAT	1080
Qy	1186	GGCTTAACTGA	CTGACTGTTTGGATGTCTTCTGAATTAAGATAAAGTGGGTTTTCCTCGAGG	1245
Db	1081	GGCTTAACTGA	CTGACTGTTTGGATGTCTTCTGAATTAAGATAAAGTGGGTTTTCCTCGAGG	1140
Qy	1246	T	1246	
Db	1141	T	1141	

RESULT 8

US-10-244-586-2

; Sequence 2, Application US/10244586

; Publication No. US20030087319A1

; GENERAL INFORMATION:

; APPLICANT: KOMES, BRUCE C.

; APPLICANT: KASOF, GARRETT M.

; APPLICANT: PROSSER, JUDITH C.

; TITLE OF INVENTION: NOVEL PROTEIN

; FILE REFERENCE: DB/009901/0270799

; CURRENT APPLICATION NUMBER: US/10/244,586

; CURRENT FILING DATE: 2002-09-16

; PRIOR APPLICATION NUMBER: US/09/594,119

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: 60/139,291

; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 843

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-244-586-2

Query Match 67.7%; Score 843; DB 5; Length 843;

Best Local Similarity 100.0%; Pred. No. 8.7e-219; Mismatches 0; Indels 0; Gaps 0;

Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	160	ATGGGACCTTAA	AGACAGTGGCCAGAGTGCCTGACCCGTGGACACAGCCGAGCACTGGGCA	219
Db	1	ATGGGACCTTAA	AGACAGTGGCCAGAGTGCCTGACCCGTGGACACAGCCGAGCACTGGGCA	60
Qy	220	GCCGGTAGTGT	TCCACGACGAGAGCGCTGTGAGACCCGCTCTCTTGGGCGACGCTGTCTCTA	279

[illegible]

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SOFTWARE: Custom
; SEQ ID NO 27357
; LENGTH: 3782
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (2200)..(2568)
; OTHER INFORMATION: 95% homologous to Homo sapiens livin inhibitor-of-
; OTHER INFORMATION: apoptosis, accession number AF311388, Smith-Waterman Score=641.
; NAME/KEY: misc feature
; LOCATION: (1)..(3782)
; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-27357

Query Match      58.6%; Score 729.8; DB 9; Length 3782;
Best Local Similarity 79.6%; Pred. No. 5.3e-188;
Matches 1033; Conservative 0; Mismatches 2; Indels 262; Gaps 4;

QY 140 TCAGAGCCAGTGTTCCTCCATGAGACCTAAAGACAGTGCCTGACCTGACCTGAGAC 199
DB 2180 TCGAGCCAGAGTTCCTCCATGAGACCTAAAGACAGTGCCTGACCTGAGAC 2239
QY 200 CACAGCCAGCCATGAGGACCGGTGATGCTCCAGCAGCAGCCGTGTGACCCGCT 259
DB 2240 CACAGCCAGCCATGAGGACCGGTGATGCTCCAGCAGCAGCCGTGTGACCCGCT 2299
QY 260 CTCTGGCAGCCCTGTCTAGGCTTGACACCTGACAGCCCTGAGACCACTGATGAGC 319
DB 2300 CTCTGGCAGCCCTGTCTAGGCTTGACACCTGACAGCCCTGAGACCACTGATGAGC 2359
QY 320 AGATCCCTGGCCAGCTGCGGCCCTCTGACAGAGAGAGAGAGAGGCGCCGAGGCCA 379
DB 2360 AGATCCCTGGCCAGCTGCGGCCCTCTGACAGAGAGAGAGAGAGGCGCCGAGGCCA 2419
QY 380 CTTTGTCCAGGGGAGCTGCTTCCCGGACATGAGGCTCTAGAGAGTTCCTTGGCTCT 439
DB 2420 CTTTGTCCAGGGGAGCTGCTTCCCGGACATGAGGCTCTAGAGAGTTCCTTGGCTCT 2479
QY 440 TCTATGACTGAGCCGCTGACTGCTGAGGTGCAACCCGAGCTGCTGCTGCGGCTTCT 499
DB 2480 TCTATGACTGAGCCGCTGACTGCTGAGGTGCAACCCGAGCTGCTGCTGCGGCTTCT 2539
QY 500 TCCACACA----- 507
DB 2540 TCCACACAGCTGACACCATGTGTGACACTGAGTTCAAGTTCAGACTCTGCCACTTCC 2599
QY 508 ----- 507
DB 2600 TGGCTGAAAGACAGGAGCAGAGGAGCCACCGAGGCTTTACAATACTGAGCACAGCATG 2659
QY 508 -----GCCATGAGCAAGTGAAGT 529
DB 2660 GTCAATTGTGACAGTGGGCTGTGGCGGAGCAACCATCTGGGCATCAGGACAAAGTGAAGT 2719
QY 530 GCTTCTTCTGCTATGAGGAGCTGACAGAGCTGGAAGCGGAGGACGACCCCTGAGAGGAGC 589
DB 2720 GCTTCTTCTGCTATGAGGAGCTGACAGAGCTGGAAGCGGAGGACGACCCCTGAGAGGAGC 2779
QY 590 ATGCCAAGTGTTCCTCA-----GCT 610
DB 2780 ATGCCAAGTGTTCCTCAAGGTACCGGCTGCCCCCTGCGGGGAGCCCGGCTGTGATCATGAGCT 2839
QY 611 GTCAAGTCTGCTCCGGCTCAAAAGAGAGACTTTGTCCACAGTGTGACAGAGACTCACT 670
DB 2840 GTCAAGTCTGCTCCGGCTCAAAAGAGAGACTTTGTCCACAGTGTGACAGAGACTCACT 2899
QY 671 CCGAGCTCTGAGGCTCTGAGACCCGTGAGAAAGAACCGGAGAGACGACGCCCTGTGAGGCC 730
DB 2900 CCGAGCTCTGAGGCTCTGAGACCCGTGAGAAAGAACCGGAGAGACGACGCCCTGTGAGGCC 2959
QY 731 CCTCGTCCCTGCTCTGAGGTAACCTGAGCTGCCACCCAGAGAGAGAGTTCAGTCTG 790
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DB 2960 CTTCC----- 2964
QY 791 AAGTCCAGAGAGCCAGAGACAGAGATGTGAGAGCGAGCTGCGGCGCTGACAGAGG 850
DB 2965 -----GAGCCAGAGAGATGTGAGAGCGAGCTGCGGCGCTGACAGAGG 3007
QY 851 AAGAGACGTGCAAGTGTGCTGAGACCGGCGCGGTGTCACTGCTTTGTGCGGTGCGGCC 910
DB 3008 AAGAGACGTGCAAGTGTGCTGAGACCGGCGCGGTGTCACTGCTTTGTGCGGTGCGGCC 3067
QY 911 ACTGCTGTGCTGAGTGTGCCCCGAGCTGACCTGAGCCCATCTGACAGAGGCCCGG 970
DB 3068 ACTGCTGTGCTGAGTGTGCCCCGAGCTGACCTGAGCCCATCTGACAGAGGCCCGG 3127
QY 971 TCCGACCCGCTGCGGACCTTCTCTGTAGGCGAGGTGCATAGGCCAGC 1029
DB 3128 TCCGACCCGCTGCGGACCTTCTCTGTAGGCGAGGTGCATAGGCCAGC 3187
QY 1030 CTGCAAGTGGGCTCCCTGCCCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1089
DB 3188 CTGCAAGTGGGCTCCCTGCCCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3247
QY 1090 GAGTGCAGAGCTGTGTCTCATCCAGACAGTACAGCCCTGATTCGCCGACACCGGCCA 1149
DB 3248 GAGTGCAGAGCTGTGTCTCATCCAGACAGTACAGCCCTGATTCGCCGACACCGGCCA 3307
QY 1150 GGGTGGAGAGAGAGCCCTTGTGCGGTGGGGAGTGAAGCTTAAGTGAATG 1209
DB 3308 GGGTGGAGAGAGAGCCCTTGTGCGGTGGGGAGTGAAGCTTAAGTGAATG 3367
QY 1210 CTTGTAATGAAATAAGTGGGTTTCCCTGAGAGT 1246
DB 3368 CTTGTAATGAAATAAGTGGGTTTCCCTGAGAGT 3404

RESULT 10
US-10-203-708-22
; Sequence 22, Application US/10203708
; Publication No. US20030149238A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/10/203,708
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatsSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-708-22

Query Match      54.2%; Score 675; DB 6; Length 769;
Best Local Similarity 91.2%; Pred. No. 3.6e-173;
Matches 769; Conservative 0; Mismatches 0; Indels 74; Gaps 2;

QY 160 ATGGAGCTTAAAGACAGTGCAGAGCTGACCCGTGACACACAGCCAGGCCATGAGGCA 219
DB 1 ATGGAGCTTAAAGACAGTGCAGAGCTGACCCGTGACACACAGCCAGGCCATGAGGCA 60
QY 220 GCCGATGATGCTCCACGAGAGAGCCGTGTGACCCCGCTCTCTGAGGAGCCCTGTGCTTA 279
DB 61 GCCGATGATGCTCCACGAGAGAGCCGTGTGACCCCGCTCTCTGAGGAGCCCTGTGCTTA 120
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QY 280 GGCTGACACCTGACAGAGCTGAGACCACTGTGATGAGGAGATCTGAGGCGACCTGCGG 339
Db 121 GGCTGACACCTGACAGAGCTGAGACCACTGTGATGAGGAGATCTGAGGCGACCTGCGG 180
QY 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
Db 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 400 TTCCCGGACATGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
Db 241 TTCCCGGACATGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 460 GCTAGAGTGCACCCGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTG 519
Db 301 GCTAGAGTGCACCCGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTG 360
QY 520 AAGGTGAGTGTCTTCTGCTATGAGGAGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 579
Db 361 AAGGTGAGTGTCTTCTGCTATGAGGAGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 420
QY 580 TGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
Db 421 TGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 478
QY 640 GACTTTGTCCACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699
Db 479 GACTTTGTCCACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 538
QY 700 GAAGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
Db 539 GAAGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 574
QY 760 CTGGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
Db 575 -----GAGCCAGAGAGAT 586
QY 820 GTGAGAGCGAGCTGCGAGCGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
Db 587 GTGAGAGCGAGCTGCGAGCGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 646
QY 880 GCGGTGTTCATGCTTTTGTGCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939
Db 647 GCGGTGTTCATGCTTTTGTGCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 706
QY 940 CTGAGAGCTGAGCCCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
Db 707 CTGAGAGCTGAGCCCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 766
QY 1000 TAG 1002
Db 767 TAG 769

RESULT 11
US-10-723-860-8265
; Sequence 8265, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8265
; LENGTH: 858
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-723-860-8265
Query Match 51.4%; Score 640.6; DB 8; Length 858;
Best Local Similarity 98.6%; Pred. No. 8e-164;
Matches 646; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 589 CATGCCAATGTGTTCCTCCAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 648
Db 175 CATCTCGGGGACATCTGACAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
QY 649 CACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 708
Db 235 CACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294
QY 709 GAAGAGCAGACCCCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 768
Db 295 GAAGAGCAGACCCCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 354
QY 769 CCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 828
Db 355 CCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
QY 829 CAGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 888
Db 415 CAGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
QY 889 ATGCTCTTTTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 948
Db 475 ATGCTCTTTTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
QY 949 TGCCCATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1008
Db 535 TGCCCATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 594
QY 1009 TGCCATGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1068
Db 595 TGCCATGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 654
QY 1069 ACTGTGTTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
Db 655 ACTGTGTTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 714
QY 1129 TGAATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1188
Db 715 TGAATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774
QY 1189 TTAACGTGACCTGTTGATGCTTGAATAGAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1243
Db 775 TTAACGTGACCTGTTGATGCTTGAATAGAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 829

RESULT 12
US-10-723-860-4448
; Sequence 4448, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4448
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-723-860-4448

Query Match 47.4%; Score 590; DB 8; Length 676;
Best Local Similarity 98.9%; Pred. No. 4.4e-150;
Matches 607; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

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OY 637 AGAGACTTTGTCACAGTGTGACAGAGACTCACTCCAGCTGAGGCTCTGGAGACCG 696
DB 34 AGAGACTTTGTCACAGTGTGACAGAGACTCACTCCAGCTGAGGCTCTGGAGACCG 93
OY 697 TGGGAGAACCGGAGAGACGAGCCGCTGAGCCCTCCCTGCTGCTGCTGCTGCTGCT 756
DB 94 TGGGAGAACCGGAGAGACGAGCCGCTGAGCCCTCCCTGCTGCTGCTGCTGCTGCT 153
OY 757 GAGCTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTCCAGAG-----CCAG 809
DB 154 GAGCTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTCCAGAGACCCCTGAG 213
OY 810 AGCAGAGAGATGTGAGAGCGAGCTGCGCGCTGCGAGAGAGAGAGAGAGAGTGTG 869
DB 214 AGCAGAGAGATGTGAGAGCGAGCTGCGCGCTGCGAGAGAGAGAGAGAGAGTGTG 273
OY 870 CTTGAGACCGGCGCTGTCATCGTCTTGTGCGGTGCGGCACTGCTGCTGCTGCTG 929
DB 274 CTTGAGACCGGCGCTGTCATCGTCTTGTGCGGTGCGGCACTGCTGCTGCTGCTG 333
OY 930 TGCCCCGCGCTGAGCTGTGCCCCATCTGCAAGAGCCCCGCTGCGAGCGCTGCGAC 989
DB 334 TGCCCCGCGCTGAGCTGTGCCCCATCTGCAAGAGCCCCGCTGCGAGCGCTGCGAC 393
OY 990 CTTGCTGCTGAGGCGAGGTCATGAGCGCGGCGAGGTCGCTGCAAGTGGCTCTCTG 1049
DB 394 CTTGCTGCTGAGGCGAGGTCATGAGCGCGGCGAGGTCGCTGCAAGTGGCTCTCTG 453
OY 1050 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109
DB 454 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 513
OY 1110 ATCCAGAGACTGACCAAGCCCTGATTCCTCCGACCAAGGCTGAGAGAGAGCCCT 1169
DB 514 ATCCAGAGACTGACCAAGCCCTGATTCCTCCGACCAAGGCTGAGAGAGAGCCCT 573
OY 1170 GCTTGGCGTGGAGAGTGTGCTTACCTGTTGAGTCTTGAATTAAGTAAAGT 1229
DB 574 GCTTGGCGTGGAGAGTGTGCTTACCTGTTGAGTCTTGAATTAAGTAAAGT 633
OY 1230 GGGTTTCCCTGGA 1243
DB 634 GGGTTTCCCTGGA 647
```

RESULT 13

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US-10-203-708-21
; Sequence 21, Application US/10203708
; Publication No. US20030149238A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1068
; TYPE: DNA
```

; ORGANISM: Homo sapiens
US-10-203-708-21

Query Match 43.0%; Score 535.2; DB 6; Length 1068;
Best Local Similarity 75.8%; Pred. No. 3.4e-135;
Matches 810; Conservative 0; Mismatches 33; Indels 225; Gaps 3;

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OY 160 ATGGAGCTTAAGACAGATGCAAGTCCGTGACCCGTGACCAAGCCGAGCCACTGGACA 219
DB 1 ATGGAGCTTAAGACAGATGCAAGTCCGTGACCCGTGACCAAGCCGAGCCACTGGACA 60
OY 220 GCCGATGATGATCCAGCAGAGAGGCTGTGAGACCCGCTCTGTGGAGAGCCCTGTCTTA 279
DB 61 GCCGATGATGATCCAGCAGAGAGGCTGTGAGACCCGCTCTGTGGAGAGCCCTGTCTTA 120
OY 280 GGCCTGGAACCTGAGAGCCTGAGACCAAGTGTGAGAGAGAGTCTGAGCAGCTGAG 339
DB 121 GGCCTGGAACCTGAGAGCCTGAGAGCCTGAGAGCAGTGGAGATCTGGGCAAGCTGAG 180
OY 340 CCGCTGACAGAGAGAGAGAGAGAGAGGCGCGGAGCCACCTTGTCCAGGAGGCTTGGC 399
DB 181 CCGCTGACAGAGAGAGAGAGAGAGAGGCGCGGAGCCACCTTGTCCAGGAGGCTTGGC 240
OY 400 TTCCCGGCAATGGGCTGTGAGAGATGTGAGCTGTGAGCTCTTCTAATGACTGGCCGCTACT 459
DB 241 TTCCCGGCAATGGGCTGTGAGAGATGTGAGCTGTGAGCTCTTCTAATGACTGGCCGCTACT 300
OY 460 GCTGAGGTGCAACCCGAGCTGCTGAGCTGCGGCTTCTTCAACAAGCCATCAGAGAC 519
DB 301 GCTGAGGTGCAACCCGAGCTGCTGAGCTGCGGCTTCTTCAACAAGCCATCAGAGAC 360
OY 520 AAGGTGAGGTGCTTCTTCTGATAGGAGGCTGTGAGAGCTGAGAGCCGAGGAGACACCC 579
DB 361 AAGGTGAGGTGCTTCTTCTGATAGGAGGCTGTGAGAGCTGAGAGCCGAGGAGACACCC 420
OY 580 TGAACGAGCATGCAAGTGTGCTCCAGCTGTGAGTCTGCTGCTGCTGCTGCTGCTGCT 639
DB 421 TGAACGAGCATGCAAGTGTGCTCCAGCTGTGAGTCTGCTGCTGCTGCTGCTGCTGCT 480
OY 640 GACTTGTGCAACATGTGCAAGAGACTCACTCCAGTGTGAGGCTGCTGCTGCTGCTGCT 689
DB 481 GACTTGTGCAACATGTGCAAGAGACTCACTCCAGTGTGAGGCTGCTGCTGCTGCTGCTGCT 540
OY 690 ----- 689
DB 541 ACCTCTCCTGGGCTCCGGGTGAGAGTCTGCCCCCTCTAATTTCCCAAGGCTT 600
OY 690 -----GGAACCGTGGAGAGAACCGAGAGACGACGCCCTGTGAG 728
DB 601 GATGATCTGTGCTCTTCCAGGACCGGTGAGAGAACCGAGAGACGACGCCCTGTGAG 660
OY 729 CCGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
DB 661 CCGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
OY 745 ----- 744
DB 721 GAGGCTGAGGAGAGGAGGCTGAGAGACCCGACCTTCAATGAGCCATAGAGGTGAG 780
OY 745 -----TGTGGTACCTGAGCTGAGCTGCAACCCAGAGAGAGTCCAGTCTGAAGTGTG 796
DB 781 GAGGAGGTGTGAGGACATTTCCAGAGGCTGCTGCTGAGAGGAGTCAATCAGCGAG 840
OY 797 CCGAGAG-----CCAGAGCCAGAGAGTGTGAGGCGAGCTGAG 834
DB 841 GCCAGAGGCGCTGAGGCTTCTTGAAGCCCAAGAGCCAGAGATGTGAGGCGAGCTGAG 900
OY 835 CGGCGCTGAGAGAGAGAGAGAGAGTGTGCTGAGACCGGCGCTGTCTCAATGCTC 894
DB 901 CGGCGCTGAGAGAGAGAGAGAGAGTGTGCTGAGACCGGCGCTGTCTCAATGCTC 960
OY 895 TTGTGCGGTGAGGCACTGCTGTGTGAGTGTGCTGAGTGTGCTGAGCTGTGAGCTGAGCTG 954
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Db 961 TTTTGGCGGTGGGACCACTGTCGTCTAGTGTGCCCCCGGCGCTGCAGCTGTGCCCC 1020

Oy 955 ATCTGCAGAGCCCCCGTCGCGAGCGCGGTGGCGACCTTCTGTCTAG 1002
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1021 ATCTGCAGAGCCCCCGTCGCGAGCGCGGTGGCGACCTTCTGTCTAG 1068

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RESULT 14
US-10-188-646-11
; Sequence 11, Application US/10188646
; Publication No. US2004000555A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobbe
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 11
; LENGTH: 4810
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-188-646-11

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Query Match	39.5%	Score 492.4	DB 6	Length 4810
Best Local Similarity	99.8%	Pred. No. 1.6e-123		
Matches 493, Conservative	0	Mismatches 1	Indels 0	Gaps 0

Qy	19	GGAGAGCCTGTGCTTATTCCTGTGTGCCAAGGTGGAGCCCGAGGGGTCAAGAGCTCCAG	78
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Qy	79	AAGGGCCAGCTGGGCAATTTCTGAGATTGGCCATAGCCCCCATTTCTGTGCAAACTTG	134
Db	229	AAGGGCCAGCTGGGCAATTTCTGAGATTGGCCATAGCCCCCATTTCTGTGCAAACTTG	288
Qy	139	GTCAGAGCCAGTGTTCCTTCATGGAGACCTAAAGAAGTGGCCAAATGTGCTGACCGTGA	199
Db	289	GTCAGAGCCAGTGTTCCTTCATGGAGACCTAAAGAAGTGGCCAAATGTGCTGACCGTGA	344
Qy	199	CCAAGCCGAGCAGCTGGGCAAGCCGGTGAATGGTCCACGACAGAGCCGCTGTGGAACCCGC	258
Db	349	CCAAGCCGAGCAGCTGGGCAAGCCGGTGAATGGTCCACGACAGAGCCGCTGTGGAACCCGC	408
Qy	259	TCTCTGGGCAAGCCCTTCTCTTAGGCCCTGTGACACTTGACAGAGCCTGGAGCAAGTGAATGG	312
Db	409	TCTCTGGGCAAGCCCTTCTCTTAGGCCCTGTGACACTTGACAGAGCCTGGAGCAAGTGAATGG	466
Qy	319	CAGATCCTGGGCAAGCTGGGCAAGCCCTGACAGAGAGGAAGAGAGAGGAGCGCCGGAGCC	378
Db	469	CAGATCCTGGGCAAGCTGGGCAAGCCCTGACAGAGAGGAAGAGAGAGGAGCGCCGGAGCC	522
Qy	379	ACCTTGTCCAGGGGGGCGCTTCTCCCGGCAATGGGCTCTGAGGAATGGCTGTGGCTTCC	438
Db	529	ACCTTGTCCAGGGGGGCGCTTCTCCCGGCAATGGGCTCTGAGGAATGGCTGTGGCTTCC	588
Qy	439	TTCTATGACGTGAGCGGCTGACGTGCTGAGGTGACCAACCGAGCTGTGGCTGTGCAGCTTC	498
Db	589	TTCTATGACGTGAGCGGCTGACGTGCTGAGGTGACCAACCGAGCTGTGGCTGTGCAGCTTC	644
Qy	499	TTTCCACACAGGCCA 512	
Db	649	TTTCCACACAGGTCA 662	

RESULT 15
US-10-723-860-4697
; Sequence 4697, Application US/1072386C
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natacha

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; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4697
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; LENGTH: 449
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; TYPE: DNA
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; ORGANISM: Homo sapiens
;
US-10-723-860-4697

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Query Match	36.0%;	Score 449;	DB 8;	Length 449;
Best Local Similarity	100.0%;	Pred. No. 8	3e-112;	
Matches 449;	Conservative 0;	Mismatches 0;	Gaps 0	

QY	160	ATGGGACCTTAAAGACAGTGCCTCAAGTGCCTGCACCTGTGACACAGCCAGCCACATGGGGCA	215
Db	1	ATGGGACCTTAAAGACAGTGCCTCAAGTGCCTGCACCGTGGACCAAGCCAGCCATCTGGGGCA	60
QY	220	GCCGGTGAATGTGCTCCACGCGAGGAGCGCTGTGGAATCCCGGCTCTTGTGGGACGCTGTGCTTA	275
Db	61	GCCGGTGAATGTGCTCCACGCGAGGAGCGCTGTGGAATCCCGGCTCTTGTGGGACGCTGTGCTTA	120
QY	280	GGCCTGGAACACCTGCGAGCGCTGGGACACACGTGAGATGGGACAGATCTGTGGGCAAGCTGGG	335
Db	121	GGCCTGGAACACCTGCGAGCGCTGGGACACACGTGAGATGGGACAGATCTGTGGGCAAGCTGGG	180
QY	340	CCCCTGACAGAGAGGAAAGAGAGAGGAGCGCCGGGGCCACTTGTGCCAGGGGGCTGGCC	395
Db	181	CCCCTGACAGAGGAGGAAAGAGAGAGGAGCGCCGGGGCCACTTGTGCCAGGGGGCTGGCC	240
QY	400	TTCCTCCGGGAAATGGGCTCTGAGAGAGTTGGTGTCTGGCTCTCTTCTATATGACTGGCCGGCTGACT	455
Db	241	TTCCTCCGGGAAATGGGCTCTGAGAGAGTTGGTGTCTGGCTCTCTTCTATATGACTGGCCGGCTGACT	300
QY	460	GCTGAAGTGCACACCCGAGCTGTGCTGCTGTGCGGGCTTCTTCCACACAGGCGCATCAGAGAC	515
Db	301	GCTGAAGTGCACACCCGAGCTGTGCTGCTGTGCGGTCTGTGCCGCTTCTTCCACACAGGCGCATCAGAGAC	360
QY	520	AAGGTGAGTGTCTTCTTCTGCTATATGGGGGCTCTGCAGAGCTGAAAGCGCGGGGAGGACCTCC	575
Db	361	AAGGTGAGTGTCTTCTTCTGCTATATGGGGGCTCTGCAGAGCTGAAAGCGCGGGGAGGACCTCC	420
QY	580	TGGAGGAGAGATGCGCAAGTGTCTCCCGAG	608
Db	421	TGGAGGAGAGATGCGCAAGTGTCTCCCGAG	449

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OM nucleic - nucleic search, using sw model

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Perfect score: 1246

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15: /SIDS5/ptodata/1/pubnna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	54.2	769	US-11-135-855-22	Sequence 22, Appl
2	535.2	43.0	1068	US-11-135-855-21	Sequence 21, Appl
3	92.6	7.4	2106	US-11-136-527-2757	Sequence 2757, Ap
4	85.2	6.8	3837	US-11-136-527-2596	Sequence 2596, Ap
5	84	6.7	600	US-10-750-185-21867	Sequence 21867, A
6	84	6.7	600	US-10-750-623-21867	Sequence 21867, A
7	83.2	6.7	1097	US-10-750-185-33882	Sequence 33882, A
8	83.2	6.7	1097	US-10-750-623-33882	Sequence 33882, A
9	82.2	6.6	600	US-11-136-527-6853	Sequence 6853, Ap
10	79.6	6.4	3076	US-10-960-414-432	Sequence 432, Appl
11	67.8	5.4	5366	US-11-091-928-4	Sequence 4, Appl1
12	67.8	5.4	5984	US-11-091-928-3	Sequence 3, Appl1
13	58.8	4.7	1575	US-11-102-026A-114	Sequence 114, Appl
14	58.2	4.7	2468	US-11-136-527-303	Sequence 303, Appl
15	50	4.0	10968	US-11-075-185-35	Sequence 35, Appl
16	50	4.0	78869	US-11-075-185-1	Sequence 1, Appl1
17	48	3.9	660	US-09-925-065A-657778	Sequence 657778, A
18	47.6	3.8	1224	US-10-960-414-240	Sequence 240, Appl

19	46	3.7	2136	US-11-072-512-618	Sequence 618, Appl
20	44.6	3.6	116856	US-11-143-980-1	Sequence 1, Appl1
21	43.2	3.5	1277	US-11-096-568A-23174	Sequence 23174, A
22	43	3.5	169469	US-10-506-454-1690	Sequence 1690, Ap
23	42.8	3.4	1891	US-11-072-512-1455	Sequence 1455, Ap
24	42.2	3.4	815	US-11-096-568A-13878	Sequence 13878, A
25	42.2	3.4	1546	US-11-112-944-14	Sequence 14, Appl1
26	42.2	3.4	167891	US-11-121-086-14	Sequence 14, Appl1
27	41.6	3.3	1997	US-10-750-185-49945	Sequence 49945, A
28	41.6	3.3	1997	US-10-750-623-49945	Sequence 49945, A
29	41.6	3.3	113193	US-10-478-943D-1	Sequence 1, Appl1
30	41	3.3	1412	US-11-096-568A-17496	Sequence 17496, A
31	40.4	3.2	2589	US-11-122-329-48	Sequence 48, Appl1
32	40.2	3.2	556	US-10-301-480-42114	Sequence 42114, A
33	40.2	3.2	556	US-10-301-480-655523	Sequence 655523, A
34	40.2	3.2	2615	US-11-096-568A-24486	Sequence 24486, A
35	40.2	3.2	2615	US-11-072-512-1280	Sequence 1280, Ap
36	40	3.2	7364	US-11-096-281-10	Sequence 10, Appl1
37	39.6	3.2	1728	US-11-096-568A-10391	Sequence 10391, A
38	39.6	3.2	113193	US-10-478-943D-1	Sequence 1, Appl1
39	39.6	3.2	191684	US-11-121-086-2	Sequence 2, Appl1
40	39	3.1	3582	US-10-194-487-465	Sequence 465, Appl
41	39	3.1	3582	US-10-195-883-465	Sequence 465, Appl
42	39	3.1	3582	US-10-195-888-465	Sequence 465, Appl
43	39	3.1	3582	US-10-195-889-465	Sequence 465, Appl
44	38.8	3.1	685	US-09-925-065A-57942	Sequence 57942, A
45	38.8	3.1	685	US-10-301-480-159180	Sequence 159180, A

ALIGNMENTS

RESULT 1	US-11-135-855-22
1	Sequence 22, Application US/1135855
2	Publication No. US2005025557A1
3	GENERAL INFORMATION:
4	APPLICANT: SMITHKLINE BEECHAM P.L.C.
5	TITLE OF INVENTION: NOVEL COMPOUNDS
6	FILE REFERENCE: GP50013
7	CURRENT APPLICATION NUMBER: US/11/135,855
8	CURRENT FILING DATE: 2005-05-24
9	PRIOR APPLICATION NUMBER: US/10/203,708
10	PRIOR FILING DATE: 2002-08-13
11	PRIOR APPLICATION NUMBER: PCT/US01/04703
12	PRIOR FILING DATE: 2001-02-14
13	PRIOR APPLICATION NUMBER: 60/182,172
14	PRIOR FILING DATE: 2000-02-14
15	PRIOR APPLICATION NUMBER: 60/186,084
16	PRIOR FILING DATE: 2000-02-29
17	NUMBER OF SEQ ID NOS: 46
18	SOFTWARE: FastSeq for Windows Version 3.0
19	SEQ ID NO 22
20	LENGTH: 769
21	TYPE: DNA
22	ORGANISM: Homo sapiens
23	US-11-135-855-22
24	Query Match
25	Best Local Similarity 91.2%; Score 675; DB 14; Length 769;
26	Matches 769; Conservative 0; Mismatches 0; Indels 74; Gaps 2;
27	US-11-135-855-22
28	160 ATGGGACCTTAAGACAGAGTCCCTGACCGTGGACCAAGCGGACCACTGGGCA 219
29	
30	1 ATGGGACCTTAAGACAGAGTCCCTGACCGTGGACCAAGCGGACCACTGGGCA 60
31	
32	220 GCGGAGTATGATGCCAGCGAGGAGCGTGGACCCCGCTCTGCGGAGCCCTGCGCTTA 279
33	
34	61 GCGGAGTATGATGCCAGCGAGGAGCGTGGACCCCGCTCTGCGGAGCCCTGCGCTTA 120
35	
36	280 GCGGAGTATGATGCCAGCGAGGAGCGTGGACCCCGCTCTGCGGAGCCCTGCGCTTA 339
37	

Db		12	GACCTGGACAACCTGCAGAGACTGCGGACCACGTGGATAGGACAGATCTTGCGCCAGCTGCCG	180
Oy		340	CCCTTGAACAAGAAGAAAGAGAGAGAGAGCGCCCGAGGCACTTTGTCCAGAGGAGCCTGCC	399
Db		181	CCCCCTGACAGAGGAGGAAAGAGAGAGAGGCGCCCGAGGCACTTTGTCCAGAGGAGCCTGCC	240
Oy		400	TTCCCGGCAGTAGGAGCTCTGAGAGAGATTGGCTGGCTTCCTTTATATGACTGAGCGCTGACT	459
Db		241	TTCCCGGCAGTAGGAGCTCTGAGAGAGATTGGCTGGCTTCCTTTATATGACTGAGCGCTGACT	300
Oy		460	GCTGAGGTGCACCCCGAAGCTGTGCTGCTGCCGCTTCTTCCACACAGGCACTCAGGAC	519
Db		301	GCTGAGGTGCACCCCGAAGCTGTGCTGCTGCCGCTTCTTCCACACAGGCACTCAGGAC	360
Oy		520	AAGTGAGGTGCTTTCTTCTGCTATAGGAGGCTTGACAGACTGAAAGCGCGGAGACGACCCC	579
Db		361	AAGTGAGGTGCTTTCTTCTGCTATAGGAGGCTTGACAGACTGAAAGCGCGGAGACGACCCC	420
Oy		580	TGACAGGAGCATGCCAAGTGATTCCCAGCTGCAGTTCCTGCTCCGCTCAAAAGGAGAA	639
Db		421	TGACAGGAGCATGCCAAGTGATTCCCAGCTGCAGTTCCTGCTCCGCTCAAAAGGAGAA	478
Oy		640	GACTTTGTCCAAGTGTGACAGAGACTCACTCCAGCTGCTGGGCTCTTGAGACCCGATG	699
Db		479	GACTTTGTCCAAGTGTGACAGAGACTCACTCCAGCTGCTGGGCTCTTGAGACCCGATG	538
Oy		700	GAAAGAACCGGAAAGACGACGCCCTGTGGCCCTCCGTCCCTGTGCTTGAGTAACCTGAG	759
Db		539	GAAAGAACCGGAAAGACGACGCCCTGTGGCCCTCCGTCCCTGTGCTTGAGTAACCTGAG	574
Oy		760	CTGCCCAACACCCAGAGAGAGGTCCAGTCTGAAGTGCCCAAGGACCAAGGACAGAGAT	819
Db		575	-----GAGCCAGGAT	586
Oy		820	GTGGAAGCGCACGTGGCGGCTGCGGCTGACAGAGAGAGAGACSTGCAGAGTGTGCTTGACCG	879
Db		587	GTGGAAGCGCACGTGGCGGCTGCGGCTGACAGAGAGAGAGACSTGCAGAGTGTGCTTGACCG	646
Oy		880	GCCGTGTCATGTCCTTTGTGCGGTGCGGACCACTGATGTGCTGAGGTGACCGCCCGG	939
Db		647	GCCGTGTCATGTCCTTTGTGCGGTGCGGACCACTGATGTGCTGAGGTGACCGCCCGG	706
Oy		940	CTGCAGACTGTGCCCACTCTGCAGAGCGCCCGTCCGACGCGAGTCGACCTTCTGTGCC	999
Db		707	CTGCAGACTGTGCCCACTCTGCAGAGCGCCCGTCCGACGCGAGTCGACCTTCTGTGCC	766
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Db		767	TAG 769	
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; Sequence 21, Application US/11135855				
; Publication No. US2005025557A1				
GENERAL INFORMATION:				
APPLICANT: SMITHKLINE BEECHAM CORPORATION				
APPLICANT: SMITHKLINE BEECHAM P.L.C.				
TITLE OF INVENTION: NOVEL COMPOUNDS				
FILE REFERENCE: GP50013				
CURRENT APPLICATION NUMBER: US/11/135,855				
CURRENT FILING DATE: 2005-05-24				
PRIOR APPLICATION NUMBER: US/10/203,708				
PRIOR FILING DATE: 2002-08-13				
PRIOR APPLICATION NUMBER: PCT/US01/04703				
PRIOR FILING DATE: 2001-02-14				
PRIOR APPLICATION NUMBER: 60/182,172				
PRIOR FILING DATE: 2000-02-14				
PRIOR APPLICATION NUMBER: 60/186,084				
PRIOR FILING DATE: 2000-02-29				
NUMBER OF SEQ ID NOS: 46				
SOFTWARE: FastSeq for Windows Version 3.0				
SEQ ID NO 21				

[illegible]

QY 607 AGCTGCACTTCCTGCTCCGTCACAAAGGAGAGACTTTTCCACAGTGTGAGAGACT 666
 DB 281 AGGTGTGAGTTCTTATGATACRAATGAAGGAGGAGGAGTTGTAGTGAAGTTCAAGCCAGA 340
 QY 667 CACTCCCACTGCTGG 682
 DB 341 TATCCTCATCTTCTTG 356

RESULT 6

US-10-750-623-21867
 ; Sequence 21867, Application US/10750623
 ; Publication No. US20050287531A1
 ; GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis
 TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 FILE REFERENCE: MM1100-1
 CURRENT APPLICATION NUMBER: US/10/750,623
 PRIOR FILING DATE: 2003-12-31
 PRIOR APPLICATION NUMBER: US 60/437,482
 PRIOR FILING DATE: 2002-12-31
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 21867
 LENGTH: 600
 TYPE: DNA
 ORGANISM: Bovine MM8708049
 US-10-750-623-21867

Query Match 6.7%; Score 84; DB 8; Length 600;
 Best Local Similarity 57.4%; Pred. No. 2.8e-09;

Matches 147; Conservative 2; Mismatches 107; Indels 0; Gaps 0;

QY 427 GCTGTGCTCTCTTCTATGACTGCGCTGACTGTGAGTGCACCCGAGCTGTGCT 486
 DB 101 CGCTTGAGAACATTATGTACTGCGCATCTACTGTATCACTTACGCCAGAGCTTGA 160
 QY 487 GCTGCGGCTTCTTCCACACAGGCCATCGAGACAGGTAGGTCTTCTTGTCTATGG 546
 DB 161 AGTGTGAGTTCTATGATGATGAGTGCACAGCATGTCAAGTCTTGTGTATGCT 220
 QY 547 GGCCTGCAAGCTGGAAGCGCGGAGCAGCCCTGAGCAGAGATGCCAAGTGTCC 606
 DB 221 GGCCTTAAGGTGTGGGATCTGAGATGACCATGGGTAGAACAGCCAAATGTTCCA 280
 QY 607 AGCTGCACTTCTGCTCCGCTCAAAAGGAGAGACTTTGTCCAGTGTGAGAGACT 666
 DB 281 AGGTGAGAGTTCTTGAATGAAGGAGGAGAGTTGTAGTGAAGTTCAAGCCAGA 340
 QY 667 CACTCCCACTGCTGG 682
 DB 341 TATCCTCATCTTCTTG 356

RESULT 7

US-10-750-185-33882
 ; Sequence 33882, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis

FILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MM1100-2
 CURRENT APPLICATION NUMBER: US/10/750,185
 CURRENT FILING DATE: 2003-12-31
 PRIOR APPLICATION NUMBER: US 60/437,482
 PRIOR FILING DATE: 2002-12-31
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 33882
 LENGTH: 1097
 TYPE: DNA
 ORGANISM: Bovine 19866880491325
 US-10-750-185-33882

Query Match 6.7%; Score 83.2; DB 8; Length 1097;
 Best Local Similarity 57.8%; Pred. No. 4.4e-09;

Matches 148; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 427 GCTGTGCTCTCTTCTATGACTGCGCTGACTGTGAGTGCACCCGAGCTGTGCT 486
 DB 272 CGCTTGAGAACATTATGTACTGCGCATCTACTGTATCACTTACGCCAGAGCTTGA 331
 QY 487 GCTGCGGCTTCTTCCACACAGGCCATCGAGACAGGTAGGTCTTCTTGTCTATGG 546
 DB 332 AGTGTGAGTTCTATGATGATGAGTGCACAGCATGTCAAGTCTTGTGTATGATGCT 391
 QY 547 GGCCTGCAAGCTGGAAGCGCGGAGCAGCCCTGAGCAGAGATGCCAAGTGTCC 606
 DB 392 GGCCTTAAGGTGTGGGATCTGAGATGACCATGGGTAGAACAGCCAAATGTTCCA 451
 QY 607 AGCTGCACTTCTGCTCCGCTCAAAAGGAGAGACTTTGTCCAGTGTGAGAGACT 666
 DB 452 AGGTGAGAGTTCTTGAATGAAGGAGGAGAGTTGTAGTGAATCAAGCCAGA 511
 QY 667 CACTCCCACTGCTGG 682
 DB 512 TATCCTCATCTTCTTG 527

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US-10-750-623-33882
 ; Sequence 33882, Application US/10750623
 ; Publication No. US20050287531A1
 ; GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis
 TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 FILE REFERENCE: MM1100-1
 CURRENT APPLICATION NUMBER: US/10/750,623
 PRIOR FILING DATE: 2003-12-31
 PRIOR APPLICATION NUMBER: US 60/437,482
 PRIOR FILING DATE: 2002-12-31
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 33882
 LENGTH: 1097
 TYPE: DNA
 ORGANISM: Bovine 19866880491325
 US-10-750-623-33882

Query Match 6.7%; Score 83.2; DB 8; Length 1097;
 Best Local Similarity 57.8%; Pred. No. 4.4e-09;

Matches 148; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 427 GCTGTGCTCTCTTCTATGACTGCGCTGACTGTGAGTGCACCCGAGCTGTGCT 486
 DB 272 CGCTTGAGAACATTATGTACTGCGCATCTACTGTATCACTTACGCCAGAGCTTGA 331


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QY 487 GCTCCGCGCTCTTCCACACAGCCATCAGACAAAGTGAGTCTCTTCTGCTATGAG 546
    |||
Db 332 AGTCTGGTTTCTATTATGATGTCGACAGCATGTCAAGTCTTTTGTGTGATGCT 391
    |||
QY 547 GGCCTGACAGCTGGAAGCCGGGAGACGACCTCTGACGAGCATGTCCAACTGTTCC 606
    |||
Db 392 GGCCTTAAGTGTGGGATCTGGAGATGACCCATGGGTAGAACAGCCCAATGTTTCCA 451
    |||
QY 607 AGCTGTAGTCTCTGCTCCGCTCAAAAGAGAGACTTTTGTCCACAGTGTGACAGACT 666
    |||
Db 452 AGGTGTAGTCTTGTATGATGATGATGAAGAGGAGAGGTTTGTAGTGAATTCAGCCAGA 511
    |||
QY 667 CACTCCAGCTGCTG 682
    |||
Db 512 TATCTCATCTTCTTG 527
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RESULT 9

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US-11-136-527-6853
; Sequence 6853, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mount, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIORITY FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIORITY FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6853
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6853

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Query Match 6.6%; Score 82.2; DB 14; Length 600;

Best Local Similarity 67.8%; Pred. No. 7.1e-09; Mismatches 52; Indels 3; Gaps 1;

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QY 821 TGGAGGCGCACTGCGCGCTGACGAGAGAGAGAGAGAGAGTGTGCTGACCGCG 880
    |||
Db 119 TGGAGAGAAAGTTCGGAAGTCCAGAGAGAGAGAGAGAGTGTGATGATGACCGAG 178
    |||
QY 881 CCGTGTCTATGCTTCTTGTGCGCGTCCGCACTGCTC--TGTCTGAGTGTGCCCCG 937
    |||
Db 179 AGGCTCTCTGCTGCTTCTTCTGCTGCGCAATGCTGCTGCAAGATGTGCCCCCT 238
    |||
QY 938 GCGTGCAGTGTGCGCCATCTGACAGAGCCCGCGCCAGCCCGCTGCGGACCTTCTCT 997
    |||
Db 239 CTCTGAGAGAGTGTCCATCTGACAGAGAGATTCAGAGGACAGTGCAGCATTTCTCT 298
    |||
QY 998 CCT 1000
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Db 299 CCT 301
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RESULT 10

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US-10-960-414-432
; Sequence 432, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSH
; APPLICANT: VEGA, VINCENT B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; PRIORITY FILING DATE: 2004-10-06
; NUMBER OF SEQ ID NOS: 500

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 432
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-960-414-432

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Query Match 6.4%; Score 79.6; DB 7; Length 3076;

Best Local Similarity 57.7%; Pred. No. 2.9e-08; Mismatches 104; Indels 0; Gaps 0;

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QY 437 CCTCTATGACCTGCGCGCTGACTGTGAGTGTGACCCGAGCTGTGCTGCTGCTGCT 496
    |||
Db 1506 CATTCTTTACTGCGCCCTGATGTTCTATGATTCATCTGACAGCTTGCAAGTGGCGGTT 1565
    |||
QY 497 TCTTCCACAGCCCATCAGACAGAGTGAAGTGTCTTCTGCTATGAGGCGCTGACGA 556
    |||
Db 1566 TTTATTATGTGGTGAACAGTATGATGTCAAAATGCTTTGCTGTGATGTGAGTCTCAGGT 1625
    |||
QY 557 GCTGGAAGCGCGGGAGACCCCTGACGAGCATGCAAGTGTGCTTCCAGCTGTGCTGCT 616
    |||
Db 1626 GTTGGGATGTGAGATGATGATCCATGAGTTCACATGAGTGTGCTTCCAAAGTGTGAGT 1685
    |||
QY 617 TCTGCTCCGCTCAAAAGAGAGACTTGTCCACAGTGTGACAGAGACTCACTCCGAG 676
    |||
Db 1686 ACTTGTATGAATTTAAAGACAGAGATTCTCCGTCAAGTTCAGCCAGTTACCTTCATC 1745
    |||
QY 677 TGCTGG 682
    |||
Db 1746 TACTTG 1751
    |||

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RESULT 11

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US-11-091-928-4
; Sequence 4, Application US/11091928
; Publication No. US20050261306A1
; GENERAL INFORMATION:
; APPLICANT: JOH-E, IKEDA
; TITLE OF INVENTION: Anti-neurodegenerative agents
; FILE REFERENCE: K7-A0501P-US(CIP)
; CURRENT APPLICATION NUMBER: US/11/091,928
; PRIORITY FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP2002-286400
; PRIORITY FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 5366
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-928-4

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Query Match 5.4%; Score 67.8; DB 14; Length 5366;

Best Local Similarity 57.2%; Pred. No. 1.2e-05; Mismatches 92; Indels 0; Gaps 0;

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QY 408 CATGGCTCTGAGAGATGTGCGTGTGCTCTCTTATGACTGCGCCCTGACTGTAAGT 467
    |||
Db 1113 CTTTGCTTACGAAGAACTACGCTGACTCTTTTAAAGACTGCCCCGGGAATCAGCTGT 1172
    |||
QY 468 GGCACCGAGAGCTGCTGCTGCTGCTGCTTCTTCCACAGGCGCATCAGAGCAAGTGAG 527
    |||
Db 1173 GGGAGTTGACGACTGCGCCAAAGCAAGTCTTTTCTACACAGGTATTAAGGACTTCCTCA 1232
    |||
QY 528 GTGCTTCTTCTGATGAGGAGCTGACAGCTGGAAGCCGCGGAGACGACCTTGAACGA 587
    |||
Db 1233 GTGCTTCTTCTGAGGAGGTTTAAAGAAATGCGAGAAAGGATGATGACCATTAACGA 1292
    |||
QY 588 GATGCGAGTGTGCTTCCACAGCTGTGATGTTCTGCG 622
    |||
Db 1293 TCACACGAGATGTTTCCCAATTGTCATTTCTTC 1327
    |||

```

RESULT 12
 US-11-091-928-3
 ; Sequence 3, Application US/11091928
 ; Publication No. US20050261306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOH-E, IKEDA
 ; TITLE OF INVENTION: Anti-neurodegenerative agents
 ; FILE REFERENCE: K7-A0501P-US(CIP)
 ; CURRENT APPLICATION NUMBER: US/11/091, 928
 ; CURRENT FILING DATE: 2005-03-29
 ; PRIOR APPLICATION NUMBER: JP2002-286400
 ; PRIOR FILING DATE: 2003-09-30
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 3
 ; LENGTH: 5984
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-11-091-928-3

Query Match 5.4%; Score 67.8; DB 14; Length 5984;
 Best Local Similarity 57.2%; Pred. No. 1.2e-05;
 Matches 123; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 408 CATGGCTGTGAGAGTTCCTGCTGCTCTCTCTATGACTGGCCGCTGACTGTAGT 467
 DB 1113 CTTTGCTTACAGAGAACTACGCGCTGGACTCTTTTACGAGCTGGCCCCGGGAATCAGCTGT 1172
 QY 468 GCCACCCGAGCTGTGCTGCTGCTGCTGCTCTCTCACACAGCCCATGAGACAAAGTGA 527
 DB 1173 GGGAGTTTCAGACACTGGCCAAAGCAGAGCTTTTCTACACAGGTATTAAGACATCGTCCA 1232
 QY 528 GTGCTCTCTTCTGCTATGAGGGGCTGCGAGAGCTGAGCGGGGAGACGCCCTGAGCGGA 587
 DB 1233 GTGCTTCTCTGAGAGGGGTGTTTGAAGAAATGCGAGAGGTGATGACCATTTAGACGA 1292
 QY 588 GCATGCCAAGTGTCTCCCACTGTCACTGTTCCGCG 622
 DB 1293 TCACACCAAGATGTTTCCCAATGTCCATTTCTCC 1327

RESULT 13
 US-11-102-026A-114
 ; Sequence 114, Application US/11102026A
 ; Publication No. US20060021087A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology LLC
 ; APPLICANT: Baum, James A
 ; APPLICANT: Gilbertson, Larry A
 ; APPLICANT: Kovacic, David K
 ; APPLICANT: LaRosa, Thomas J
 ; APPLICANT: Lu, Maolong
 ; APPLICANT: Munyikwa, Tichifa R. I.
 ; APPLICANT: Roberts, James K
 ; APPLICANT: Wu, Wei
 ; TITLE OF INVENTION: Compositions and Methods for Control of Insect Infestations in Pl
 ; FILE REFERENCE: 38-21(53596)
 ; CURRENT APPLICATION NUMBER: US/11/102, 026A
 ; CURRENT FILING DATE: 2005-04-08
 ; PRIOR APPLICATION NUMBER: 60560842
 ; PRIOR FILING DATE: 2004-04-09
 ; PRIOR APPLICATION NUMBER: 60565632
 ; PRIOR FILING DATE: 2004-04-27
 ; PRIOR APPLICATION NUMBER: 60579062
 ; PRIOR FILING DATE: 2004-06-11
 ; PRIOR APPLICATION NUMBER: 60603421
 ; PRIOR FILING DATE: 2004-08-20
 ; PRIOR APPLICATION NUMBER: 60617261
 ; PRIOR FILING DATE: 2004-10-11
 ; PRIOR APPLICATION NUMBER: 60669241
 ; PRIOR FILING DATE: 2005-04-07
 ; NUMBER OF SEQ ID NOS: 190

; SEQ ID NO 114
 ; LENGTH: 1575
 ; TYPE: DNA
 ; ORGANISM: Diabrotica virgifera
 ; US-11-102-026A-114

Query Match 4.7%; Score 58.8; DB 14; Length 1575;
 Best Local Similarity 52.9%; Pred. No. 0.0012;
 Matches 126; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 427 CCGTGGCTCTCTCTATGACTGCGGCTGACTGTGAGTGCACCCGAGCTGTGCT 486
 DB 620 CGGTAGCAACATTCAGGGTGTGGCCAAAGACATTAACAGAGGCTTGTGAGTTACT 679
 QY 487 GCTGCCGCTCTCTCAACAGAGCCATGAGCAAGTGAAGTGTCTTCTGCTATGGG 546
 DB 680 GAGGGGGATTTTATTACACAGAGACTGGGAGCACAACGTGTGCTTTTATTTGTGTGG 739
 QY 547 GGCCTGCAAGCTGGAAGCGCGGAGCAGACCCCTTGACGAGCATGCCAAGTGTGCTCC 606
 DB 740 GGATTAAGAACTGGAGATGAAGAGATGATCTTGGAGCAACATGCCCTTTGGTTTAC 799
 QY 607 ACCTGTCACTTCTGCTCCGGTCAAAAGAGACCTTGTCCACAGTGTGACAGAGA 664
 DB 800 AATGTGTCTTCTCAATTTTAAAAAGGCAAGAAATTCATGATCAAGTAAAGAGA 857

RESULT 14
 US-11-136-527-303/c
 ; Sequence 303, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mount, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136, 527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574, 294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 303
 ; LENGTH: 2468
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-11-136-527-303

Query Match 4.7%; Score 58.2; DB 14; Length 2468;
 Best Local Similarity 55.8%; Pred. No. 0.0016;
 Matches 111; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 475 GAGTGTGGCTGCTGCTGCTCTCTTCCACACAGCCATCAGACAAAGTGAAGTCTTC 534
 DB 1299 GAGAGCTTGCAGAGACTGGATTTTATGCTTTAGGGAAGTGAAGTGAAGTCTTC 1240
 QY 535 TTCTGTATGGGGCTTGCAGAGCTGGAAGCGCGGGAAGACCCCTGAGCGGAGATGCC 594
 DB 1239 CACTGTGAGAGAGGGGTCAAGGATTTGAGAGCCAAAGTGAAGACCTTTGGACAGCATGCT 1180
 QY 595 AAGTGTTCCTCCAGCTGTGAGTTCCTGCTCCGCTCAAAAGAGAGACTTGTCCACAGT 654
 DB 1179 AAGTGTATTCAGGGGTGAATATCTATTGATGAGAAAGGAGCAAGATATATTAAT 1120
 QY 655 GTGCAGAGACTCACTGCC 673
 DB 1119 ATTCAATTAAACCATTTAC 1101

RESULT 15
 US-11-075-185-35
 ; Sequence 35, Application US/11075185
 ; Publication No. US2005026434A1

```
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 10968
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
; US-11-075-185-35
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Query Match 4.0%; Score 50; DB 14; Length 10968;
Best Local Similarity 48.3%; Pred. No. 0.11;
Matches 140; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
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QY 658 CAGAGACTACTCCACAGTGTGGGCTCCTGGGACCCGTGGAGAACCGAAGACGCA 717
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Db 4081 CAGAGAACCCCGGCGGGGGGTGCGCTGTGACCTGGGGCCCGGCTGTGACGCA 4140
    |||||

QY 718 GCCCTGTGGCCCCCTCGTCCCTGTGGGTACCTTGAAGTGGCCACACCCAGGAGA 777
    |||||
Db 4141 GCCCTGTGGCGGGGGGTGGGCGGCGGACGAGGCTCGCGCTGGCGGGGGGC 4200
    |||||

QY 778 GAGTCCAGTCTGAAGTGCACAGAGCCAGAGGATGTGAGGGGCGCAGCTGCCG 837
    |||||
Db 4201 GCGGCGCGCGCCACCGCTGCGCGAGGTGGCGGGCGCGCGCGACGCGACCG 4260
    |||||

QY 838 CGGCTGCAGAGAGAGACGTGCAAGTGTGCTTGACCGCGCTGTCCATGTTCTTT 897
    |||||
Db 4261 ACGGCGTGTATCCCGGCGGAGCGGTCTATCAAGGGCGGACCGGGGAGCTTGGGCGG 4320
    |||||

QY 898 GTGCCGTCGCGCACTGTGTGTGCTGAGTGTGCCCCGAGCTTGCAGCT 947
    |||||
Db 4321 CAGGTGCGCGGCACTGTGTGCGGCGCACGCGTGCAGCACTGTGCT 4370
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2006, 19:34:28 ; Search time 5744 Seconds
(without alignments)
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Title: US-09-762-577B-12
Perfect score: 1721
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: gb_dat.*
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8: gb_pr.*
9: gb_ro.*
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11: gb_sy.*
12: gb_un.*
13: gb_vi.*
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15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1713	99.5	1260	8	AF311388	Homo sapi

4	1713	99.5	1301	8	AY358835	Homo sapi
5	1713	99.5	1376	6	AX067715	Sequence
6	1694	98.4	1168	6	AF301009	Homo sapi
7	1694	98.4	1312	6	CQ896990	Sequence
8	1694	98.4	1312	6	BC014475	Homo sapi
9	1694	98.4	1337	6	BD248275	DNA encod
10	1694	98.4	1337	6	AR242238	Sequence
11	1694	98.4	1370	6	AY358836	Homo sapi
12	1547	89.9	840	6	BD167853	Survivin-
13	1547	89.9	840	6	BD153655	Survivin-
14	1547	89.9	843	6	AX067716	Sequence
15	1487.5	86.4	1021	8	AY517497	Homo sapi
16	1217	70.7	672	6	BD167852	Survivin-
17	1217	70.7	672	6	BD167854	Survivin-
18	1217	70.7	723	6	BD167851	Survivin-
19	1217	70.7	723	6	BD153653	Survivin-
20	1030	59.8	4810	8	HS4059298	Homo sapi
21	1030	59.8	184223	8	HS4261N11	Human DNA
22	1009	58.6	615	6	CQ721033	Sequence
23	543	31.6	1598	5	AF468029	Xenopus 1
24	543	31.6	1638	5	AB197251	Xenopus 1
25	489	28.4	1770	9	AF183431	Rattus no
26	489	28.4	3290	9	AF190020	Rattus no
27	487	28.3	2907	9	BC062055	Rattus no
28	482.5	28.0	1550	9	BSU79142	Sus scrofa
29	482	28.0	2341	9	BC083555	Rattus no
30	478.5	27.8	2676	6	AR106401	Sequence
31	478.5	27.8	2676	6	AR116703	Sequence
32	478.5	27.8	2676	6	BD190872	Detection
33	478.5	27.8	2676	6	AR370621	Sequence
34	478.5	27.8	2676	6	AX670908	Sequence
35	478.5	27.8	2676	9	MMU88908	Mus musc
36	478	27.8	1809	9	AF183430	Rattus no
37	477.5	27.7	1537	4	AY267257	Bob tauru
38	474.5	27.6	2278	5	AY184377	ICtalarus
39	472	27.4	2563	6	AR270513	Sequence
40	472	27.4	2563	6	AR380349	Sequence
41	472	27.4	2563	8	HUMSCP	Sequence
42	472	27.4	2563	8	BC037420	Homo sapien
43	472	27.4	2601	6	AR129833	Homo sapi
44	472	27.4	2601	6	AR606789	Sequence
45	472	27.4	2601	6	AR637717	Sequence

ALIGNMENTS

RESULT 1
LOCUS CQ896991 1260 bp DNA
DEFINITION Sequence 11 from Patent WO2004091388.
ACCESSION CQ896991
VERSION CQ896991.1 GI:55581833
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
1 Butz,K., Crnkovic-Mertens,I. and Hoppe-Seyler,F.
LIVIN-SPECIFIC SIGNAS FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS
Patent: WO 2004091388-A 11 28-OCT-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)

FEATURES
source Location/Qualifiers
1..1260
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 3.06e-85 Length: 1260
Pred. No.:

Score: 1713.00 Matches: 308
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 6 Gaps: 0

US-09-762-577B-12 (1-309) x C0896991 (1-1260)

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OY 1 MetGlyProLyAspSerAlaLySLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 174 ATGGAGACCTAAAGACAGTGTCCAAAGTGTCTGCACCTGTGACACAGCCGAGCCACTGGGCA 233
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 234 GCGGGGATGTGTCCACGAGGAGCGCTGTGGACCCGCTCTCTGGGAGCGCTGTCTTA 293
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 294 GGGCTGGACACCTGACAGACCTGGAGACAGTGGATGGGACAGATCTGGGCGACCTCGG 353
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 413
DB 354 CCCCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
OY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
DB 414 TTCCCCGCGCATGGGCTCTGAGAGATGTGTGTGGCTCTCTCTCTCTCTCTCTCTCTCTCT 473
OY 101 AlaGluValAProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlnHisGlnAsp 120
DB 474 GCTAGGGGCCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 533
OY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 534 AAGGTAGAGGTCTTCTCTGTATAGGGGCTGTGAGAGCTGAGAGCGGGGAGACGACCCC 593
OY 141 TrpThrGlnHisAlaIleTrpPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
DB 594 TGGACGAGCATGTGCAAGTGTCTCCACAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 653
OY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 654 GACTTGTTCACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 713
OY 181 GlnGlnProGlnLysAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
DB 714 GAAGAACCGGAAAGACGAGCCCTGTGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAG 773
OY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlnValAlaArgAsp 220
DB 774 CTGCCCAACCCAGAGAGAGAGTCCAGTCTGAAGTGGCCAGAGAGCGAGAGACCGAGANT 833
OY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
DB 834 GTGGAGCGCGAGCTGTGGCGGCTGTGACAGAGAGAGACCTGTGACAGTGTGTGAGCCGCG 893
OY 241 AlaValSerIleValPheValProCysGlnHisLeuValCysAlaGlnCysAlaProGly 260
DB 894 GCGGTGTTCATGCTCTTGTGTGCGGTGGCCACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 953
OY 261 LeuGlnLeuCysProIleCysArgAlaProValAlaGlySerArgValArgThrPheLeuSer 280
DB 954 CTGGAGCTGTGCCCCATCTGACAGAGCCCCCTGCCACCGCGTGCAGACCTCTGTGCC 1013
OY 281 ***AlaArgCysHisGlyArgProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 300
DB 1014 TAGGCGAGGTGCGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
OY 301 LeuPheTrpThrValPheTrpAlaCys 309
DB 1074 CTGTTCTGACACTGTGTCTGGGCTGTGC 1100
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RESULT 2

CS113085
LOCUS CS113085 1260 bp DNA linear PAT 24-JUN-2005
DEFINITION Sequence 103 from Patent WO2005054507.
ACCESSION CS113085
VERSION CS113085.1 GI:68224657
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 Corfe, B. and Chirakkal, H.
AUTHORS Gene screen
TITLE Patent: WO 2005054507-A 103 16-JUN-2005;
JOURNAL University of Sheffield (GB)
FEATURES
source location/Qualifiers
1..1260
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ALIGNMENT Scores:

Pred. No.: 3,056-85 Length: 1260
Score: 1713.00 Matches: 308
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 6 Gaps: 0

US-09-762-577B-12 (1-309) x CS113085 (1-1260)

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DB 234 GCGGGGATGTGTCCACGAGGAGCGCTGTGGACCCGCTCTCTGGGAGCGCTGTCTTA 293
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 294 GGGCTGGACACCTGACAGACCTGGAGACAGTGGATGGGACAGATCTGGGCGACCTCGG 353
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 413
DB 354 CCCCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
OY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
DB 414 TTCCCCGCGCATGGGCTCTGAGAGATGTGTGTGGCTCTCTCTCTCTCTCTCTCTCTCTCT 473
OY 101 AlaGluValAProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlnHisGlnAsp 120
DB 474 GCTAGGGGCCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 533
OY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 534 AAGGTAGAGGTCTTCTCTGTATAGGGGCTGTGAGAGCTGAGAGCGGGGAGACGACCCC 593
OY 141 TrpThrGlnHisAlaIleTrpPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
DB 594 TGGACGAGCATGTGCAAGTGTCTCCACAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 653
OY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 654 GACTTGTTCACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 713
OY 181 GlnGlnProGlnLysAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
DB 714 GAAGAACCGGAAAGACGAGCCCTGTGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAG 773
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QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlnGluProGlyAlaArgAsp 220
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Db 834 GTGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 893
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db 894 GCCCTGTCATCGCTCTTGTCCTGCGGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 953
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 954 CTGACGCTGTGCGCCATCTGAG 1013
QY 281 ***AlaArgCysHisIleGlyArgArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeu 300
Db 1014 TAGCCAGGTGCGCCATCTGAG 1073
QY 301 LeuPheThrThrValPheTrpAlaCys 309
Db 1074 CTGTTCTGACGTGTGTTCTGGGCTGC 1100

RESULT 3
AF311388 1260 bp mRNA linear PRI 29-JAN-2001
LOCUS Homo sapiens livin inhibitor-of-apoptosis (LIVIN) mRNA, complete
DEFINITION
ACCESSION AF311388
VERSION AF311388.1 GI:11245452
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Kasof, G.M., and Gomes, B.C.
TITLE Livin, a novel inhibitor of apoptosis protein family member
JOURNAL J. Biol. Chem. 276 (5), 3238-3246 (2001)
PUBMED 11024045
REFERENCE 2 (bases 1 to 1260)
AUTHORS Kasof, G.M., and Gomes, B.C.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-2000) Enabling Science and Technology,
AstraZeneca Pharmaceuticals, 1800 Concord Pike, Wilmington, DE
19803, USA

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TFLS"

ORIGIN
Alignment Scores:
Pred. No.: 3.06e-85 length: 1260

Score: 1713.00 Matches: 308
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 8 Gaps: 0
US-09-762-577b-12 (1-309) x AF311388 (1-1260)

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QY 21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 234 GCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 293
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 294 GGCCTGACACCTGACAG 353
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 354 CCCCTGACAG 413
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 414 TTCCCGGCAATGGGCTGTGAG 473
QY 101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGACACCCAG 533
QY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db 534 AAGGTAGAGGTCTTCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 593
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 594 TGACGAGAGATGCCAAGTGTCTCCCAAGTGTCAAGTGTCTCCGTTCAAAAGAGAGA 653
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db 654 GACTTGTCCACAGTGTGACAG 713
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Db 774 CTGCCCAACCCAGAGAGAGAGTCCAGTCTGAAGTCCAGAGAGAGAGAGAGAGAGAGAGAT 833
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Db 834 GTGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 893
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
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QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
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QY 281 ***AlaArgCysHisIleGlyArgArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeu 300
Db 1014 TAGCCAGGTGCGCCATCTGAG 1073
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Db 1074 CTGTTCTGACGTGTGTTCTGGGCTGC 1100

RESULT 4

AY358835
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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Homo sapiens clone DNA142232
AY358835
AY358835.1
FLI - CDNA.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1301)

REFERENCE
AUTHORS

Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Denel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Heldens,S., Huang,A., Kim,H.S., Klimovskii,L., Jin,Y., Johnson,S., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagstad,A., Vandlen,R., Velanabre,C., Weiland,D., Woode,K., Xie,M.H., Yamaura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,M.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL
PIRMBED
12973509
2 (bases 1 to 1301)
Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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Query Match: 99.5% Indels: 0
DBs: 8 Gaps: 0

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21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
275 GCCGGTAGTGGTCCACGACGAGACGCGCTGTGGACCCGCTCTCTGGGAGCCCTGTCTTA 334
41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60

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Query Match:	99.5%
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Matches:	308
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Mismatches:	1
Indels:	0
Gaps:	0

US-09-762-577B-12 (1-309) x AX067715 (1-1376)

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Db	211	ATGGGACCTTAAGAAGACGTGCCAAGTCCCTGCACCCGTGGACACAGCCGAGCACTGAGCA	270
QY	21	AlaGlyAspGlyProThrGlnGlnLysCysGlyProArgSerLeuGlySerProValLeu	40
Db	271	GCCGGTAGTGTCCACGACGAGAGCGCTGTGAGACCCCGCTCTGTGGGAGCCCTGTCTTA	330
QY	41	GlyLeuAspThrCysArgAlaTrpAspH1sValAspGlyGlnH1sLeuGlyGlnLeuArg	60
Db	331	GGCCTGGACACCTGGAGAGCCTGGAGACACGTGAGTGGCAATCTCTGGACGCTGGCG	390
QY	61	ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	80
Db	391	CCCCGACAG	450
QY	81	PheProGlyMetGlySerGlyGlnLysLeuArgLeuAlaSerPheTrpAspTrpLeuThr	100
Db	451	TTCCCCGGGCAATGGGCTCTGAGGAGTGGCTGTGGCTCTCTCTATGACATGGCGCGTACT	510
QY	101	AlaGlnValProProGlnLysLeuLeuLysAlaAlaGlyPhePheH1sThrGlyH1sGlnAsp	120
Db	511	GCTAGAGTGCACCCGACGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	570
QY	121	LysValAlaArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgLysAspAspPro	140
Db	571	AAGGTGAGGTGCTCTTCTTCTGTCTATGGGGGCTGCAGAGCTGGAAGGCGGGGAGCA	630
QY	141	TrpThrGlnH1sAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg	160
Db	631	TGGACGGAGCATGCCAAGTGTGTCCCGACGCTGTCACTTCTCTCCGGTCAAAAGGAAACA	690
QY	161	AspPheValH1sSerValGlnGlnThrH1sSerGlnLeuLeuGlySerTrpAspProTrp	180
Db	691	GACTTTGTCCACAGTGTGCAGAGAGACTCACTCCAGCTGCTGGCTCTCTGGAGCCCGTGG	750
QY	181	GlnGlnLysProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln	200
Db	751	GAAGAAACCGGAAAGCGACGCCCTGTGGGCCCTCCGCTCCGCTGTGGATACCTGTAG	810
QY	201	LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyLysAlaArgAsp	220
Db	811	CTGCGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTGGCCAGAGAGCGACAGAGAGAT	870
QY	221	ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	240
Db	871	GTCGAGGCGGCGAGCTGCGCGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	930
QY	241	AlaAlaSerLysLeuValPheValProCysGlyH1sLeuValCysAlaGlnCysAlaAlaProGly	260
Db	931	GCCGCTGCATCGCTTTGTGGCGGCGAGCACCTGTGCTGTGAGAGTGCACCCCGGCG	990
QY	261	LeuGlnLeuCysProLysCysArgAlaProValArgSerArgValArgThrPheLeuSer	280
Db	991	CTGCAGCGTGGCCCATCTGCAGAGAGCCCGCGTCCGAGCGCGGTGGAGCACTTCTCTGTCC	1050
QY	281	***AlaArgCysH1sGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCys	300

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Qy 301 LeupheTTrpThrValPheTrpAlaCys 309
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1111 CTGTTCTGSACTGTGTTCTGGGCGCTGC 1137

AF301009	1168 bp	mRNA	linear	PRI 05-DEC-2000
LOCUS	AF301009	Homo sapiens inhibitor of apoptosis protein KIAA mRNA, complete cds.		
DEFINITION	AF301009			
ACCESSION	AF301009.1	GI:11545502		
VERSION				

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Best Local Similarity:	94.2%
Query Match:	98.4%
DB:	8
	Gaps: 1
	Length: 1168
	Matches: 308
	Conservative: 0
	Mismatches: 1
	Indels: 18
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US-09-762-577B-12 (1-309) X AF301009 (1-1168)

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Qy 21 AlAGLYApGcYPrOThrGtGlnbArGcGLYPrOAGrGserLeuGLYserProValIeu 40
Db 61 GCCGGrGmArGrGTrCCAGCGAGAGCGCTGrGrsAGCCCGCTCTCTrGAGGACGCCCTGrGCTTA 120

[illegible]

AUTHORS		TITLE		JOURNAL		PATENT		DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OEFFENTLICHEN RECHTES (DKFZ)	
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Best Local Similarity:		94.2%		Mismatch:		1			
Query Match:		98.4%		Indels:		18			
DB:		6		Gaps:		1			
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QY	21	AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu	40						
DB	209	GCCGTGATGATCCACACAGAGACCGCTGTGACCCCGCTCTCTGGGACAGCCCTGTCTTA	268						
QY	41	GlyLeuAspThrCysArgAlaArgAspHisValAspGlyGlnLeuGlyGlnLeuArg	60						
DB	269	GGCCTGGACACTGCAGAGCCTGGGACCACTGGATGGAGATCTCGGCCAGCTGGCG	328						
QY	61	ProLeuThrGlnGluGlnGluGlnGluGlyAlaGlyAlaThrLeuSerArgGlyProAla	80						
DB	329	CCCTGCACAGAGGAGAGAGAGAGAGAGAGGCGCGGCGCACCTTGTCCAGGGGCGCTGCC	388						
QY	81	PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheThrAspTrpProLeuThr	100						
DB	389	TTCCCGGCAATGGGCTGTGAGGAGTTGCGTCTGGCCCTCTTCATGACTGGCGCTGACT	448						
QY	101	AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120						
DB	449	GCTAGAGGTGCACCCGAGCTGTGGCTGGCTGGCGGCTCTTCCACACAGGCATCAGAC	508						
QY	121	LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro	140						
DB	509	AAAGTGAAGTGTCTTCTTCTGCTATGGGGGCTTCAAGCTGGAAGCGCGGAGCAGACCC	568						
QY	141	TrpThrGlnHisAlaIleYsrTrpPheProSerCysGlnPheLeuLeuArgSerIleArg	160						
DB	569	TGGACGAGCATGCAAGTGTGTCCCAAGCTGCAGTTCTCTGCTCCGCTCAAAAGAGAGA	628						
QY	161	AspPheValHisSerValGlnGlnIleThrHisSerGlnLeuLeuGlySerTrpAspProTrp	180						
DB	629	GACTTTTCCACAGTGTGTCAGAGACTCACTCCACACTCTCTGGGCTCTCTGGAGACCCGAG	688						
QY	181	GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln	200						
DB	689	GAAAGAACCGGAAGCGAGCCCTGTGGCCCTCTCGCTCTTGGAGTACCTTGAAG	748						
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QY	216	-----ProGlyAlaArgAspValGln	222						
DB	809	CCAGCCCAAGCCCAAGAGGCGTGTGGGTCTTTGAGACCCCAAGAGCCAGGAGATGTGAG	868						
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DB	869	GCCACACTGGGCGGTGACAGAGAGAGAGAGAGTCTCAAGAGTGTGCTTGAACCGGCGGTG	928						

Oy		243	SerriValAPheValProCysglYhisLeuAlaCysalagluCYsaLAsgluCYsaLAProGlyIleugln	262	
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Oy		263	LeucCyProlieCYsarYAALAProVALArgSerArGYalaArgThrPhelAueSer**Ala	282	
Dd		989	CTGnccccCATcTCGAGAgaGAcCCCcgTCgcGAGccGcGrngCcCACTTCtGTgnCTnaAGccc	1046	
Oy		283	ArgCyBHIsgLYARGPrGrgLyGLyleugInsergrYLyeuProALAProLeuCysLeuPhe	302	
Dd		1049	AGgggccATTgCGccGcCACgTrGGcGTGCAGAGrGGGCTCCtCGccCTCTcGTGCTgTTC	1108	
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Dd		1109	TGGACTGTCTTCTGGGcCTGC	1129	
RESULT #	8				
LOCUS	BCL014475				
DEFINITION	Homo sapiens baculoviral IAP repeat-containing 7 (lavin)				
VERSION	BC014475				
KEYWORDS	MGC:				
SOURCE	GMC.				
ORGANISM	Homo sapiens (human)				
REFERENCE	AUTHORS				
	Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaeter,C.F., Bat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stepleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Scheetz,T.E., Brownstein,W.J., Udell,T.B., Toehiyki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.T., Bosak,S.A., McSwan,P.J., McEramon,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Woley,K.C., Hale,S., Garcia,A.M., Gay,L.U., Hulky,S.W., Vialation,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodrigues,A.C., Greenwood,J., Schmuth,I., Myers,R.M., Buttefield,Y.S., Krzyzinski,M.I., Skalska,U., Smilins,D.E., Smerench,A., Schein,J.E., Jones,S.J. and Merre,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences <i>Proc. Natl. Acad. Sci. U.S.A.</i> 99 (26), 16899-16903 (2002) 12477932				
JOURNAL PUBLISHED REFERENCE AUTHORS JOURNAL TITLE COMMENT					
		2	(bases 1 to 1312) Strauberg,R. Direct Submission Submitted (17-SRP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/DTF CDNA Library Preparation: Rubin Laboratory CDNA Sequencing Arrayed by: The I.M.A.-G.E. Consortium (LMU) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcsc.bc.ca		
			Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guan, Nancy Liao,		

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Db	209 GCCGGTGAATGTCTCCACGACGAGGCGGTGTGAACCCCGCTCTTGGGCAACCCCTGTCTTA 268
QY	41 GlyLeuAspThrCysArgAlaIatPAspRHisValAspGlyValIleLeuGlyGlnLeuArg 60
Db	269 GGCCTGGACACTGGACAGCCCTGGACCAACGTGGATGGGAGATCTCGGGCCAGCTGCCG 328
QY	61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db	329 CCCCTGACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 388
QY	81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db	389 TTCCCCGGCATGGGCTCTGAGAGATTGCGCTTGGCTCTTCTTATTAATCTGGCCGCTGACT 448
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Percent Similarity:	94.2%	Conservative:	0		
Best Local Similarity:	94.2%	Mismatches:	1		
Query Match:	98.4%	Indels:	18		
DB:	6	Gaps:	1		
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QY	21	AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu	40		
Db	230	GCGGGGAGTGGTCCACCCAGAGAGCGCTGTGACCCCGCTCTCTGGGAGCCCTGTCTTA	289		
QY	41	GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleuGlyGlnLeuArg	60		
Db	290	GGCTCTGGACACTGTGACAGCTGTGGGACCACTGTGATGGCAGATCTGGGCGACGTGGG	349		
QY	61	ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	80		
Db	350	CCCCCTGACAG	409		
QY	81	PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTyrProLeuThr	100		
Db	410	TTCCCCGGGCAATGGGCTGTGAGAGATTCGCTGTGCTCTCTCTCTCTCTCTCTCTCTCT	469		
QY	101	AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120		
Db	470	GCTGAGGAGCCACCCAGAGCTGTGGCTGGCTGGCGGCTTCTTCACACAGGCCATCAGAC	529		
QY	121	LeuValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrValArgGlyAspAspPro	140		
Db	530	AAAGTGAAGTCTTCT	589		
QY	141	TyrThrGlnHisAlaIleTyrPheProSerCysGlnPheLeuLeuArgSerTyrGlyArg	160		
Db	590	TGGACGGAGCATGCGCAAGTGTCTCCACAGCTGCAGTTCCTGCTCCGCTCAAAAGAGAA	649		
QY	161	AspPheValHisSerValGlnGlnIleThrHisSerGlnLeuLeuGlySerTyrAspProTyr	180		
Db	650	GACTTTGTCCACAGTGTGACGAGAGACTTCACCTCCACCTCTCTGGGCTTGGGACCCGTGG	709		
QY	181	GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln	200		
Db	710	GAAAGAACCGAGAGACGAGCCCTGTGGCCCTCTCCGTCTCTGAGTCTGAGTACCTTAG	769		
QY	201	LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGln-----	215		
Db	770	CTGGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTGCACAGAGCCAGAGAGAGGTCACT	829		
QY	216	-----ProGlyAlaArgAspValGlu-----	222		
Db	830	CCAGCCGAGGCCACAGAGGCGTGTGGGTTCTTTGAGCCCCACAGAGCCAGAGGATCTTGAG	889		

OY	223	AlaGlnLeuAArgxIeGlnGlnIuGTrGTrCyAluValCyAluAspAArgAlaVal	242
Dp	890	GCGCAGCTCCGGCGCGCTGCAGAGAGAGAGAGCTGCAGAGTGTGCTGGACCGCCCGTG	949
OY	243	SerTlIeValPheValProCyAsGlyIhIleuValCyAlaGluCyAlaIProGlyIeGln	262
Dp	950	TTCATCATGCTTTGTTGTCCTCGCGCGCCACCTGGTGTGTGTGATGTGGTCCCGCGCTGTGAG	1009
OY	263	LeuCySPProIleCyAsArgAlaProValArgSerArgValArgTrPheLeuSer**Ala	282
Dp	1010	CTGTGCCCCCATCTGCAGAGAGCCCCCTCCGCGACCGCGTGGCAGCCTTCTGTGCTTAGGCC	1066
OY	283	ArgCySHisGlyArgProGlyIeGlyIeGlnIleSerGlyIeAsProAlaIProLeuCyAluPhe	302
Dp	1070	AGGTGCCCATGGCCGGGCCAGGTGGGTGTGCAGAGTGGGCTCCCTGCCCCCTCTGTGCTGTTC	1128
OY	303	TrpThrValPheTrpAlaCys	309
Dp	1130	TGGACTGTGTTCTGGGCTTGC	1150

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ACCESSION	AR242238			
VERSION	AR242238.1	GI:27288060		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 1337)			
AUTHORS	Deng, G., Lin, J.-H. and Moren, M.J.			
TITLE	DNA encoding a novel human inhibitor-of-apoptosis protein			
JOURNAL	Patent: US 6472172-A 1 29-OCT-2002;			

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Best Local Similarity:	94.2%	Mismatches:	1
Query Match:	98.4%	Indels:	18
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US-09-762-577B-12 (1-309) X AR242238 (1-1337

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Db 290 GGCCTGGACACTGACAGCCTGGAGACACAGTGGATGGGCAATCCTGGGCCAGCTGGG 349

Dy 61 ProLeuThrGluGluGluGluGluGlyAlaGlyIatHleuSeAArgGlyProLa 80
Db 350 CCCCTGCACAGGAGAGAAGAGGGCGCCGGGCACTTGTCCAAGGGGCTGCC 409

DY 81 PheProGlyIyMetGlySerGlucInLeuArgLeuAlaSerPheThyAspTrpProLeuThr 100
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QY	121	LyxValAaagCysPhePheCysTyTG1G1GlyLeuGlnSerTPbYaaG1YaaPhePro	140
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QY	161	AspPheValH1sSerValG1G1UThrH1sSerGlnLeuG1SerTyrPheAppProTrp	180
Db	650	GACTTTGTCCACAGTGTGCAGAGACTACTCCAGCTGTGTGGCTCTTTGGACCCCGTGG	709
QY	181	GIUgluIPProG1uaPheAlaAlaAProValAlaProSerValProAlaSerG1YTrProGlu	200
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243 SerIleValPheValProCysGlyHisIleuValCysAlaGluCysAlaProGlyLeuGln 262

263 LeucylProlineCysArgAlaProValArgSerArgValArgPheLeuSer***Ala 282

LD 1010 C1A1GCCCCATCTGACAGACCCCCCGCCAGCCGCGAGCCACCTTCCCTGCTTACGAC 106

QY 263 ARGCSYSHISGLYARGPROGLYGLYLEUGINSERCTYLEUPROALPROLEUCYSEUPHE 302

DB 1070 AGGAGCCACGGCCCGGCCAGGTGGCTGCAGAATGGGTCCTCCTGCCCCCTCTGCTGTTC 112

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REFERENCE
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AUTHORS
Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Dowd, P., Eaton, D., Foister, J., Grimaldi, C., Gu, Q., Haas, P.E.,
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,

TITLE Goddard, A., Wood, W. I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins
A Bioinformatics Assessment

JOURNAL
PUBMED 12975309
REFERENCE 2 (bases 1 to 1370)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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Alignment Scores:
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Query Match: 98.4% Indels: 18
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QY 101 AlaGluValProProGluLeuLeuAlaAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
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DB 1175 TGGACTGTGTTCTGGGCTGCG 1195

RESULT 12
BD167853
BD167853
LOCUS Survivin-like polypeptide and its DNA. 840 bp. DNA. linear. PART 17-JAN-2003
DEFINITION BD167853
ACCESSION BD167853.1 GI:27873665
VERSION WO 0233071-A/5.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 840)
Tanaka,H. and Kaleda,I.
Survivin-like polypeptide and its DNA
Patent: WO 0233071-A 5 25-APR-2002;
TAKEDA CHEMICAL INDUSTRIES LTD,HIROSHI TANAKA, ISAO KAIEDA
OS Homo sapiens (human)
PN WO 0233071-A/5
PD 25-APR-2002
PF 16-OCT-2001 WO 2001P009071
PR 17-OCT-2000 JP 00P 316721,20-DEC-2000 JP 00P 386809 PI
HIROSHI TANAKA, ISAO KAIEDA
PC
C12N15/09, C12N15/12, C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C07K16/18, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, PC
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ORIGIN

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 Best Local Similarity: 100.0%
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Length: 840
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US-09-762-577B-12 (1-309) x BD167853 (1-840)

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QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
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 DEFINITION Survivin-like polypeptide and its DNA.
 ACCESSION BD185365

VERSION BD185365.1 GI:31877565
 KEYWORDS JP 2002355062-A/5.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 840)

REFERENCE Tanaka,H. and Kaieda,I.
 TITLE Survivin-like polypeptide and its DNA
 JOURNAL Patent: JP 2002355062-A 5 10-DEC-2002;
 COMMENT TAKEDA CHEMICAL INDUSTRIES LTD

COMMENT

OS Homo sapiens (human)
 PN JP 2002355062-A/5
 PD 10-DEC-2002
 PP 16-OCT-2001 JP 2001318533
 PT HIROSHI TANAKA, ISAO KAIEDA
 PC C12N15/09,A61K31/7088,A61K38/55,A61K39/395,A61K39/395,A61K48/
 PC 00,A61P35/00,
 PC A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19, PC
 C12N1/21,
 PC C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50, PC
 G01N33/53,
 PC G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64
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 FH Key Location/Qualifiers
 FT source 1..840 /organism='Homo sapiens (human)'.
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FEATURES

source

ORIGIN

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 Best Local Similarity: 100.0%
 Query Match: 89.9%

Length: 840
 Matches: 280
 Conservative: 0
 Mismatches: 0
 Indels: 0
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US-09-762-577B-12 (1-309) x BD185365 (1-840)

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Db 1 ATGGGGCCTAAAGACAGTGGCCAGTGTCTGACCGTGACACAGCCGAGCCACTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCyGlyProArgSerLeuGlySerProValLeu 40
Db 61 GCCGGTATGGTCCACAGCAGAGAGCGCTGTGACCCCGCTCTCGGGCAGCCCTGTCTTA 120
QY 41 GlyLeuAspThrCySAArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 121 GGCTTGACACCTGACAGCCTGGGACCACTGGATGGAGATCTTGGGCGACGCTGG 180
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QY 101 AlaGlyValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
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LOCUS Sequence 2 from Patent W00077201.
DEFINITION AX067716.1 GI:12329603
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
1 Gomes, B. C., Kasof, G. M. and Prosser, J. C.
Living, inhibitor-of-apoptosis protein-3 (Iap-3)
Patent: WO 0077201-A 2 21-DEC-2000;
Astrazeneca AB (SE)
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 89.9% Indels: 0
DB: Gaps: 0

US-09-762-577B-12 (1-309) x AX067716 (1-843)

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QY 41 GlyLeuAspThrCySArgAlaThrhAspHhSValAspGlyGInIleLeuGlyGInLeuArg 60
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QY 61 ProLeuThrhGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
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QY 81 PheProGlyMetGlySerGInGluLeuArgLeuAlaSerPheTyPAspTTPProLeuThrh 100
Db 241 TTCCCGGATGAGCTGTGAG 300
QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHhSThrhGlyHhSLeuPhe 120
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Db 361 AAGGTGAGGTGCTTCTTGTGCTATGAGGAGGCTGCAGAGCTGGAAGCGGAGAGAGAGAG 420
QY 141 TPTThrgluHhEAlAlvYtPheProSerCySgInPheLeuLeuAArgSerLySgLYArg 160
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Db 661 GTGAGAGGCGACGCTGCGGCGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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RESULT 15
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LOCUS Homo sapiens baculoviral IAP repeat-containing 7 (BIRC7) mRNA,
DEFINITION complete cde, alternatively spliced.
ACCESSION AY517497
VERSION AY517497.1 GI:41387694
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
1 (bases 1 to 1021)
Li, H., Ke, R., Wang, C., Zhou, G., Shen, C., Lin, L. and Yang, S.
Direct Submission
Submitted (03-JAN-2004) Guangzhou Fulenggen Co., Ltd., 5/F.,
Guangzhou Entrepeneur Park for Overseas Chinese Scholars, 11
Baoshi Rd., GERPD, Guangzhou, Guangdong 510730, China
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ORIGIN

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 Best Local Similarity: 82.1% Mismatches: 1
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 DB: 8 Gaps: 1

US-09-762-577B-12 (1-309) x AY517497 (1-1021)

QY 1 MetGlyProIysaPseSerAlaIysCyseLeuHisArgGlyProGlnProSerHisTrpAla 20
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 Db 61 GCCGGTATGATGTCACGACGAGAGCGCTGTGACCCCGCTCTGGGCAAGCCCTGTCTTA 120
 QY 41 GlnLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 Db 121 GGCTTGACACCTGCAAGCCTGGGACCACTGATGAGCAGATCTGGGCGACCTGCGG 180
 QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
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 QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
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 Db 361 AAGGTGAGTGTCTTCTTCTGCTATGGGGCTGCGAGCTGGAGCGCGGGAGACGACCCC 420
 QY 141 TrpThrGlnHisAlaIysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
 Db 421 TGGACGGAGCATGCAAGTGGTCCCAAGCTGATGCTTCTGCTCGGTCAAAAGAGAGA 480
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 Db 481 GACTTGTGTCCAGTGTGACAGAGACTCACCTCCAGCTGCTGGGCTCTCTGGAGACCCG 540
 QY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200
 Db 541 GAAGAACCGAAGACGAGCCCTGTGGCCCTCTCCGCTCTGAGGTACCTTAG 600
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QY 215 ----- 215
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 QY 216 ----- ProGlyAlaArgAspVal 221
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 QY 241 aValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGlyLe 261
 Db 901 CGTGTCCATGCTCTTGTGTGCGGCTGCGGCACTGTGTGTGAGTGTGCTGCTGCTG 960
 QY 261 GlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
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Search completed: April 20, 2006, 01:24:35
 Job time : 5749 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2006, 19:31:48 ; Search time 684 Seconds
(without alignments)
3010.804 Million cell updates/sec

Title: US-09-762-577b-12
Perfect score: 1721
Sequence: 1 MGPBDSAKCLHGRGPQPSHMA.....GLOSGLPAPLPLFTVFWAC 309

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4996997 seqs, 3332346308 residues
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: geneseqn2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1713	99.5	1260	12	ADH89535 Human liv
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5	1713	99.5	1376	4	AA24856	Aaf24856 Nucleotid
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7	1694	98.4	1332	10	ACC72843	ACC72843 Human can
8	1694	98.4	1332	13	ADH71344	ADH71344 Human liv
9	1694	98.4	1337	3	AA261210	AA261210 DNA encod
10	1694	98.4	1363	3	AAAI5007	AAAI5007 DNA encod
11	1694	98.4	1363	13	ADH88075	ADH88075 Human pro
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13	1547	89.9	833	4	AA24857	AA24857 Survivin-
14	1489.5	86.5	3782	5	AA591553	AA591553 Nucleotid
15	1372.5	79.8	769	4	AA216365	AA216365 DNA encod
16	1354	78.7	1068	4	AA216364	AA216364 Human SBh
17	1217	70.7	672	6	AAI42857	AAI42857 Survivin-
18	1217	70.7	723	6	AAI42856	AAI42856 Survivin-
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21	914.5	53.1	615	4	AAH99228	AAH99228 Human pro
22	913	53.1	1531	10	ADH17464	ADH17464 Mouse IL-
23	867	50.4	858	12	ADQ25445	ADQ25445 Human sof
24	846	49.2	449	12	ADQ21877	ADQ21877 Human sof
25	791.5	46.0	676	12	ADQ21628	ADQ21628 Human sof
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33	472	27.4	2563	13	ADS83635	ADS83635 Human lym
34	472	27.4	2601	2	AAT61591	AAT61591 Human c-I
35	472	27.4	3076	2	AAT72712	AAT72712 Human inh
36	472	27.4	3076	2	AA241005	AA241005 Human cel
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ALIGNMENTS

RESULT 1	ADH89535	ADH89535 standard; DNA; 1260 BP.
ID	ADH89535;	
AC	ADH89535;	
XX		
DT	22-APR-2004 (first entry)	
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DE	Human Livin DNA.	
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KM	hyperproliferative disorder; aberrant apoptosis; human; ds; Livin; gene.	
OS	Homo sapiens.	
XX		
PN	US2004005565-A1.	
XX		
PD	08-JAN-2004.	
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PF	02-JUL-2002; 2002US-00188646.	
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PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Bennett CF, Dobie KW;	
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DR	WPI; 2004-098436/10.	
XX		
DR	P-PSDB; ADH89685.	

XX New antisense oligonucleotide, having a sequence targeted to a nucleic
 PT acid encoding livin, useful for preparing a composition for treating
 PT hyperproliferative disorder or aberrant apoptosis.

PS Example 13; SEQ ID NO 4; 60pp; English.

XX The invention relates to an antisense oligonucleotide targeted to a
 CC nucleic acid encoding livin and that specifically hybridizes with the
 CC nucleic acid encoding livin and inhibits expression of livin. The
 CC antisense oligonucleotide is useful for preparing a composition for
 CC treating hyperproliferative disorder or aberrant apoptosis. The present
 CC sequence represents human livin DNA.

XX Sequence 1260 BP, 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.95e-104	Length:	1260
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DB:	12	Gaps:	0

US-09-762-577B-12 (1-309) x ADH89535 (1-1260)

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QY	61	ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	80
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DB	414	TTCCCGGACATGGGCTCTGAGAGAGTTCGCTGCTCTCTCTCTCTCTCTCTCTCT	473
QY	101	AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120
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QY	141	TTPThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGly	160
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QY	181	GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln	200
DB	714	GAAGAACCGGAG	773
QY	201	LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyValArgAsp	220
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QY	221	ValGlnValGlnLeuArgArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	240
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QY	301	LeuPheTTPThrValPheTTPAlaCys	309
DB	1074	CTGTTCTGGACTGTGTCTGGGCTGCTG	1100
RESULT 2			
ID	AEA36171	standard; DNA, 1260 BP.	
AC	AEA36171;		
XX	25-AUG-2005	(first entry)	
DE	Human nucleic acid sequence #103.		
KM	Screening; gene expression; colorectal tumor; colitis; Crohns disease;		
KW	irritable bowel syndrome; gastrointestinal disease; cytostatic;		
OS	gastrointestinal-gen.; antiinflammatory; de.		
PN	Homo sapiens.		
XX	MO2005054507-A2.		
PD	16-JUN-2005.		
PF	03-DEC-2004; 2004WO-GB005078.		
PR	04-DEC-2003; 2003GB-00028048.		
PA	(UTSH-) UNIV SHEFFIELD.		
PI	Corfe B, Chirakkal H;		
XX	WPI; 2005-435407/44.		
DR			
XX			
PT	Screening for nucleic acid molecules exhibiting altered expression in		
PT	cells grown in the presence of butyrate, and detection of the nucleic		
PT	acid molecules or the encoded polypeptides in diagnosing colorectal		
PT	cancer.		
PS	Disclosure; Page 143; 26pp; English.		
XX			
CC	The invention relates to a method of screening for nucleic acid molecules		
CC	that show altered expression in a first cell sample comprising comparing		
CC	the gene expression profile of the sample with that of a second reference		
CC	sample, where the first sample has been grown in the presence of butyrate		
CC	or a related carbon source from which butyrate is directly or indirectly		
CC	derived, but the reference sample has not. The invention also relates to		
CC	a method of detecting at least one nucleic acid molecule associated with		
CC	the initiation and/or progression of colorectal cancer in an animal,		
CC	comprising providing a biological sample comprising at least one cell to		
CC	be tested, contacting the sample with a ligand (preferably a hybridizing		
CC	nucleic acid molecule) which binds to at least one nucleic acid and		
CC	detecting the presence of at least one molecule in the sample, a method		
CC	and/or progression of colorectal cancer in an animal comprising providing		
CC	a biological sample comprising at least one cell to be tested, contacting		
CC	the sample with at least one ligand that specifically binds at least one		
CC	polypeptide encoded by a nucleic acid or a variant polypeptide comprising		
CC	an amino acid sequence which varies by the addition, deletion or		
CC	substitution of at least one amino acid residue and detecting the		

presence of the polypeptide in the sample, a method of screening for agents that modulate the activity of at least one polypeptide encoded by a gene associated with the initiation and/or progression of colorectal cancer comprising forming a preparation comprising at least one polypeptide encoded by a nucleic acid or a variant polypeptide comprising at least one addition, deletion or substitution and at least one agent to be tested and determining the activity of the agent with respect to activity of the polypeptide, and an antibody or its effective binding portion identified by the method, for use as a pharmaceutical. The methods are useful for screening for nucleic acid molecules that show altered expression in a cell sample, and for detecting a nucleic acid and a polypeptide respectively, that are associated with the initiation and/or progression of colorectal cancer and are useful for detecting or monitoring colorectal cancer, especially adenocarcinoma. The methods are also useful for screening for agents that modulate the activity of at least one polypeptide encoded by a gene associated with the initiation and/or progression of cancer, where agents identified by the method are useful for treating colorectal cancer. The methods could also be used to detect or monitor other conditions such as colitis, Crohn's disease or irritable bowel syndrome, as a screening tool for fiber consumption, as an assay for colon microflora functionality or for early detection of pre-cancerous growth. This sequence represents a human nucleic acid identified by the screening method of the invention.

Sequence 1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,95e-104	Length:	1260
Score:	1713.00	Matches:	308
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	99.5%	Indels:	0
DB:	14	Gaps:	0

US-09-762-577B-12 (1-309) x AEA36171 (1-1260)

1 MetGlyProlyAspSerAlaLeuValLeuHisArgGlyProGlnProSerHisAla 20
174 ATGGAGCTTAAGACAGTGCCTGACCGTGGACCAAGCCGAGCCAGCTGGGCA 233
21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
234 GCCGGTAGTGCTCCAGCAGAGAGAGGCGCGGGGCCACCTTGTCACGGGGCCCTGCC 293
41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnLeuGlnLeuArg 60
294 GGCTTGAACACCTGCAAGCTGGAGCCACGTGATGGCAATCTGGGCGACCTCGG 353
61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
354 CCCCTGACAG 413
81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
414 TTCCCGCGCATGGGCTCTGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
101 AlaGlnValAlaProProGlnLeuLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
474 GCTGAGGTGCAACCGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 533
121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysAlaGlyAspAspPro 140
534 AAGGTGAGGTGCTCTTCTGCTATGGGGGCTGTGAGAGCTGGAAGCCCGGGAGAGAGAG 593
141 TrpThrGlnHisAlaAlaTyrTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
594 TGAACGAGATGATGCAAGTGTCTCCCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 653
161 AspPheValHisSerValGlnGlnGlnThrHisSerGlnLeuLeuGlnGlnGlnGlnGln 180
654 GACTTTTCCACAGCTGTGCAAGAGACATCTCCACAGCTGTGCTGCTGCTGCTGCTGCT 713
181 GlnGlnProGlnLeuAlaAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200

|||||
Db 714 GAAGAACGGAGACGACGACCCCTGTGGCCCCCTCCCTGCTGCTGGGTACCTGAG 773
Gy 201 LeuProThrProArgAlaGlyValAlaGlnSerGlnSerLysAlaGlnGlnProGlyAlaArgAsp 220
Db 774 CTGCCACACCCAGAGAGAGAGTCCAGTGTGAAGTCCAGAGAGCCAGAGCCAGGAT 833
Gy 221 ValGlnAlaGlnLeuArgAlaGlyLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 834 GTGAGGCGGAGCTGCGCGCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
Gy 241 AlaValSerIleValPheValProCysGlyHisIleValCysAlaGlnCysAlaProGly 260
Db 894 GCGGTGCATGCTTTGTGGCGTGGGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 953
Gy 261 LeuGlnLeuCysProIleCysAlaGlnAlaProValArgSerArgValArgThrPheLeuSer 280
Db 954 CTGACGCTGGCCCATCTGCAAGAGCCCGCTCCGAGCGCGTGGCCACCTTCCTGTC 1013
Gy 281 ***AlaArgCysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCys 300
Db 1014 TAGCCAGGTGCTCATGCGCCGAGAGGTGGCTGCAAGTGGCTCCTGCTGCTGCTGCT 1073
Gy 301 LeuPheTrpThrValPheTrpAlaCys 309
Db 1074 CTGTTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1100

RESULT 3

ACCT2844
ID ACC72844 standard; cDNA; 1268 BP.

XX ACC72844;

DT 09-JUL-2003 (first entry)

DE Human cancer related protein encoding cDNA SEQ ID NO:182.

KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosiis; gene; ss.

OS Homo sapiens.

PN WO2003025138-A2.

XX 27-MAR-2003.

PP 17-SEP-2002; 2002MO-US029560.

XX 17-SEP-2001; 2001US-0323469P.

PR 20-SEP-2001; 2001US-0323887P.

PR 13-NOV-2001; 2001US-0350666P.

PR 08-FEB-2002; 2002US-0355145P.

PR 08-FEB-2002; 2002US-0355257P.

PR 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;

PI Zlotnick A;

XX WPI; 2003-354600/33.

DR P-Psdb; ABR58693.

XX New genes that are up-regulated or down-regulated in cancers, useful as

PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as

PT therapeutic targets for screening drugs for treating these diseases.

XX Claim 8; Page 725-726; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which

CC comprises the sequence of any of the genes that are up-regulated or down-

CC regulated in specific cancers (e.g. about 1031 genes up-regulated in

CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer

CC related gene nucleotide sequences which encode the proteins given in
 CC ABR8521 to ABR8709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies

SQ Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.96e-104 Length: 1268
 Score: 1713.00 Matches: 308
 Percent Similarity: 99.7% Conservative: 0
 Best Local Similarity: 99.7% Mismatches: 1
 Query Match: 99.5% Indels: 0
 DB: 10 Gaps: 0

US-09-762-577B-12 (1-309) x ACC72844 (1-1268)

QY 1 MetGlyProLysAspSerAlaLysCysAluHisArgGlyProGlnProSerHisTrpAla 20
 Db 174 ATGGACCTTAAGACATGCGCAAGTCTGCACTGAGACACAGCGACCTGAGCA 233
 QY 21 AlaGlySerGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 Db 234 GCCGGTATGCTCCACGACGAGCGCTGTGACCCCGCTCTCGGGACGCTGTCTTA 293
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
 Db 294 GGCTTGACACCTGCAAGCCCTGGAGCACAGTGAATGGAGCATCTGGCCGACGCTGG 353
 QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 Db 354 CCCCTGACAG 413
 QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
 Db 414 TTCCCGGCAATGGGCTCTTGAAGATTGCGTGGCTCTCTTATGACTGGCGCTGACT 473
 QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 Db 474 GCTGAAGTGCACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
 QY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
 Db 534 AAGGTAGGTGCTTCTTCTGCTATGGGGCTGCAAGAGTGAAGGGCGGGACCAACCC 593
 QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerGlyArg 160
 Db 594 TGGACGGAACATGCAAGTGTCTCCCACTGTCAAGTTCTCTCCGCAAAAGAGAGA 653
 QY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
 Db 654 GACTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGCTGGGCTCTGGGACCCGTGG 713
 QY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
 Db 714 GAAGAAACCGAAGACGACAGCCCTGTGGCCCTCCGCTCGCTCGGTGACCTCTAG 773
 QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlnAlaArgAsp 220
 Db 774 CTGCCACAGCCACGAGAGAGAGTCCAGTCTGAAAGTGGCCAGAGCCAGAGCCAGGAT 833

QY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
 Db 834 GTGAGAGCGGACGTGGGGGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
 QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
 Db 894 GCGGTTCATGCTCTTTTGTGGCGGGGACACCTGTGTGTGTGTGTGTGTGTGTGTGT 953
 QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 Db 954 CTGCACTGTGCCCCATCTGACAGAGCCCGTCCGACGCGGTGCGACCTTCTGTTC 1013
 QY 281 ***AlaArgCysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuGly 300
 Db 1014 TTAGCCAGGTGCCATGAGCCGCGCAGGTGGCTGACAGAGTGGGCTCTGCGCTCTGCG 1073

QY 301 LeuPheTrpThrValPheTrpAlaCys 309
 Db 1074 CTGTTCTGACCTGTGTCTTCTGGGCTTGC 1100

RESULT 4
 AD571346
 ID AD571346 standard; DNA; 1268 BP.
 AC AD571346;
 XX
 DT 16-DEC-2004 (first entry)
 XX

DE Human livin beta splice variant DNA.
 XX

KW Immune response; cancer-associated inhibitor of Apoptosis-family protein;
 KW IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma;
 KW human; livin beta; gene; de; immunostimulant; cytostatic.
 OS Homo sapiens.

Key Location/Qualifiers
 FH 174..1016
 FT /*tag= a
 FT /product= "Human livin beta splice variant protein"
 PN US2004192631-A1.

PD 30-SEP-2004.
 XX
 XX 24-MAR-2004; 2004US-00807897.
 PF
 XX 24-MAR-2003; 2003US-0457009P.
 PR

XX (XIAN/) XIANG R.
 PA (ZHOU/) ZHOU H.
 PA (REIS/) REISFELD R A.
 XX

PI Xiang R, Zhou H, Reisfeld RA;
 XX

DR WPI; 2004-689881/67.
 DR P-PSDB; AD571347.
 DR REFSEQ; NM_022161.
 XX

PT New DNA vaccine comprising a cancer-associated inhibitor of Apoptosis-
 PT family protein immunosuppressive gene product, useful for eliciting an immune
 PT response against cancer.
 XX

XX Claim 26; SEQ ID NO 28; 84p; English.
 PS

CC The present invention relates to a DNA vaccine effective for eliciting an
 CC immune response against cancer cells which comprises a DNA construct
 CC operably encoding at least one cancer-associated inhibitor of Apoptosis-
 CC family protein (IAP-family protein) and at least one immunosuppressive gene
 CC product in a pharmaceutical carrier. The invention is useful for treating
 CC cancer such as lung cancer, colorectal cancer and melanoma. The present
 CC sequence is the human livin beta splice variant DNA.
 XX

Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;

Alignment Scores:

Score:	1.96e-104	Length:	1268
Pred. No.:	1713.00	Matches:	308
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	99.5%	Indels:	0
DB:	13	Gaps:	0

US-09-762-577b-12 (1-309) x ADS71346 (1-1268)

```

QY 1 MetGlyProLyAspSerAlaLyCySLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 174 ATGGGACCTAAAGACAGTGCAGAGCTGCTGACCGGTGACCTCTCTGGGACGCTGTCTA 233
QY 21 AlAGLyAspGlyProThrGlnGlnGlnArgCyAGLyProArgSerLeuGlySerProValLeu 40
Db 234 GCCGTATAGTGTCCACGAGAGAGCGCTGTGACCCGCTCTCTGGGACGCTGTCTA 293
QY 41 GlyLeuAspThrCyAsArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 294 GGCTGACACCTGACAGAGCTGGAGACCACTGATGGGACAGTCTCTGGGACGCTGCG 353
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY 81 PheProGlyMetGlySerGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 414 TTCCCGGCAATGGGCTCTGAGAGAGTTCGCTGCTCTCTCTCTCTCTCTCTCTCTCT 473
QY 101 AlAGLyValProProGlnLeuLeuAlaAlaGlyPhePheHisTrpGlyHisGlnAsp 120
Db 474 GCTGAGTGTCCACCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
QY 121 LyValAlaGlyCyAsPhePheCyTyGlyGlyLeuGlnSerTrpLyAsArgLyAspAspPro 140
Db 534 AAGGTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 593
QY 141 TrpThrGlnHisAlaAlaTrpPheProSerCySglnPheLeuLeuArgSerLyGlyArg 160
Db 594 TGGACGAGAGATGCAGAGTGGTCCCGAGCTGTCTGCTGCTGCTGCTGCTGCTGCTG 653
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db 654 GACTTTTCCACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713
QY 181 GlnGlnGlnProGlnAlaAlaAlaProValAlaProSerValProAlaSerGlyTyProGln 200
Db 714 GAAGAACCGGAAGACGACGCCCTGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 773
QY 201 LeuProThrProArgArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 220
Db 774 CTGCCACACCGAGAGAGAGAGTCCAGTCTGAAAGTCCCGAGGAGCAGAGAGCAGGAT 833
QY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 834 GTGGAGGCGAGCTGCGGCGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY 241 AlaValSerIleValPheValProCySgLyHisIleValCySAlaGlnCySAlaProGly 260
Db 894 GCCGTGTCCATCGCTTTGTGCGGTGCGGCACTGTGTCTGTGTGTGTGTGTGTGTGTG 953
QY 261 LeuGlnLeuCySProIleCySArgAlaProValArgSerArgValAlaGlnPheLeuSer 280
Db 954 CTGACAGCTGTGCCCATCTGACAGAGCCCGCTCGCAGCGCGCGCGCCACCTCTGTCC 1013
QY 281 **AlaArgCySHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCyS 300
Db 1014 TAGGCGAGGTGCGCATGAGCGGAGGTGGGCTGACAGAGTGGGCTCTGCTGCTCTGTGC 1073
QY 301 LeuPheTrpThrValPheTrpAlaCyS 309

```

Db 1074 CTGTTCTGAGCTGTGTCTGAGGCTGC 1100

RESULT 5

AAAF24856

ID AAF24856 standard; cDNA; 1376 BP.

XX AAF24856;

DT 20-APR-2001 (first entry)

DE Nucleotide sequence of an apoptosis inhibitor designated livin.

KW Livin; apoptosis inhibitor; IAP-3; cancer; apoptosis; gene therapy;

KW melanoma; Alzheimer's disease; Parkinson's disease; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 211..1053

FT /tag= a

FT /product= "livin"

PN W0200077201-A1.

PD 21-DEC-2000.

PF 09-JUN-2000; 2000MO-GB002272.

PR 15-JUN-1999; 99US-0139291P.

PA (ASTR) ASTRAZENECA AB.

PA (ASTR) ASTRAZENECA UK LTD.

PT Gomes BC, Kasof GM, Prosser JC;

DR WPI; 2001-122843/13.

DR P-PSDB; AAB31478.

PT Novel livin polypeptides and polynucleotides useful for treating

PT pathophysiological disorders related to apoptosis, cancers, particularly

PT melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gene

PT therapy.

PS Claim 8; Page 53-54; 62pp; English.

XX The present sequence encodes a human polypeptide, designated livin. Livin

CC is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in

CC certain cancer cell lines and prevents apoptosis. The livin polypeptide

CC is useful for identifying compounds that inhibit and modulate livin

CC function and activity. Such compounds are useful in the treatment of a

CC dysfunctional apoptosis condition. Livin polypeptides are useful as a

CC source of probes and primers, and in gene therapy. Livin polypeptides and

CC polynucleotides, their inhibitors and modulators are useful for treating

CC pathophysiological disorders related to apoptosis, cancers, particularly

CC melanoma cancer, Alzheimer's disease and Parkinson's disease

Sequence 1376 BP; 233 A; 432 C; 454 G; 257 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.14e-104	Length:	1376
Score:	1713.00 <td>Matches:</td> <td>308</td>	Matches:	308
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	99.5%	Indels:	0
DB:	4	Gaps:	0

US-09-762-577b-12 (1-309) x AAF24856 (1-1376)

```

QY 1 MetGlyProLyAspSerAlaLyCySLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 211 ATGGGACCTAAAGACAGTGCAGAGCTGCTGACCGGTGACCTCTCTGGGACGCTGTCTA 270

```


[illegible]

XX	US2004005565-A1.
PN	08-JAN-2004.
XX	02-JUL-2002; 2002US-00188646.
PX	02-JUL-2002; 2002US-00188646.
PF	(ISIS-) ISIS PHARM INC.
XX	Bennett CF, Doble KW;
PI	WPI; 2004-098436/10.
DR	P-PsDB; ADH89543.
XX	New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
PT	Example 15; SEQ ID NO 12; 60bp; English.
PS	The invention relates to an antisense oligonucleotide targeted to a CC
CC	nucleic acid encoding Livin and that specifically hybridizes with the CC
CC	nucleic acid encoding Livin and inhibits expression of Livin. The CC
CC	antisense oligonucleotide is useful for preparing a composition for CC
CC	treating hyperproliferative disorder or aberrant apoptosis. The present sequence represents human Livin DNA.
XX	
SQ	Sequence 1168 BP; 206 A; 357 C; 393 G; 212 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	3.25e-103 Length: 1168
Score:	1694.00 Matches: 308
Percent Similarity:	94.2% Conservative: 0
Best Local Similarity:	94.2% Mismatches: 1
Query Match:	98.4% Indels: 18
DB:	12 Gaps: 1
US-09-762-577B-12 (1-309) x ADH89543 (1-1168)	
OY	1 MetGlyProLysAspSerAlaLeuCySLeuHisArgGlyProGlnProSerHisTrpAla 20
Db	1 ATGGAGCCTTAAGAACAAGTCCCAAGTCCTCGACACCCTGGACCAAGCCAGCCTGGGA 60
OY	21 AlaGlyAspGlyProThrGlnGluAryGyGlyProArgSerLeuGlySerProValIeu 40
Db	61 GCCCGATATGTATCCACGCAGAGCCCTGTGACCCCGCTCTCTGGGAGCCCTGTCTTA 120
OY	41 GlyLeuAspThrCysArGlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db	121 GGCTGGAGCACCTGGAGAGCCTGGACCAACGTGATGGAGAGATTCTGGGCCAGTTGGG 180
OY	61 ProLeuThrGlnGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgIlyProAla 80
Db	181 CCCCTACAG 240
OY	81 PheProGlyMetGlySerGluGluGluLeuArgLeuAlaSerPheIyrAspTrpProLeuThr 100
Db	241 TTCCTCCGGCATGGGCTCTTAGAGAGTTGGCTCTGGCTCTCTCTATGACTGGCCCTGACT 300
OY	101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db	301 GCAGAGAGTCCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 360
OY	121 LysValArgCysPhePheCysThrGlyGlyGluGlnIleGlnIleGlnIleGlnIleGln 140
Db	361 AAGGTAGAGTCTTCTTCTTGCTGATAGGGGGGCTTCACAGAGCTGAAGCGGGGAGAGCCC 420
OY	141 TrpThrGlnHisAlaLeuSerTrpPheProSerCysGlnPheLeuLeuArgSerIlyArg 160
Db	421 TGAGCGAGAACAGCCAAAGTGTCCCCCAGCTGATGTTCTGCTCCGGTCAAAGGAGAGA 480

QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrPaspProTyr 180
 Db 481 GACTTGTTCACAGTGTCCAGAGACTCCTCCAGGCTGTGGGCTTGGAGCCCGTGG 540
 QY 181 GlnGluProGluuAaPheValAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
 Db 541 GAAAGACCGGAAAGCGAGCCCTGTGGCCCTCCCTCCCTGCTGCTGCTGCTGCTGAG 600
 QY 201 LeuProThrProAArgArgGluValGlnSerGlnSerAlaGlnGlu----- 215
 Db 601 CTGCTCCACACCCAGAGAGAGTCTCAGTCTTAAGTGTCCAGAGCCAGAGGAGGCTAGT 660
 QY 216 -----ProGlyAlaArgPaspValGlu 222
 Db 661 CCAGCCGAGGCCAGAGGGCGTGGTGGTCTTGAAGCCCGAGAGGCGAGAGTGGAG 720
 QY 223 AlaGlnLeuArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 242
 Db 721 GCGCAGCTGCGCGCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 QY 243 SerIleValPheValProCysGlyHisIleValCysAlaGlnCysAlaProGlyLeuGln 262
 Db 781 TCCATTCCTTGTGCGGTGGCCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 QY 263 LeuCysPheProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer***Ala 282
 Db 841 CTGTGCCCCCATCTGCAGAGAGCCCGCTCGCAGCCGCGCTGCTCTCTCTAGGCC 900
 QY 283 ArgCysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCysLeuPhe 302
 Db 901 AGGCGCATGCGCGCGCGAGGCTGCGAGAGTGGGCTCCCTGCTCTGCTGCTGCTGCT 960
 QY 303 TrpThrValPheTyrPalaCys 309
 Db 961 TGGACTGT 981

RESULT 7
 ACCT2843
 ID ACC72843 standard; cDNA; 1322 BP.
 XX
 AC ACC72843;
 XX
 XX
 DT 09-JUL-2003 (first entry)
 XX
 DE Human cancer related protein encoding cDNA SEQ ID NO:181.
 XX
 KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 XX heart disease; atherosclerosis; endometriosis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W02003025138-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002W0-US029560.
 XX
 PR 17-SEP-2001; 2001US-0323469P.
 XX 20-SEP-2001; 2001US-0323887P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 08-FEB-2002; 2002US-0355145P.
 PR 08-FEB-2002; 2002US-0355257P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KB;
 PI Zlotnick A;
 XX
 DR WPI: 2003-354600/33.
 DR P-PSDB; ABR58692.
 XX
 PT New genes that are up-regulated or down-regulated in cancers, useful as

PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 PT therapeutic targets for screening drugs for treating these diseases.
 XX
 PS Claim 8; Page 725; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
 CC related gene nucleotide sequences which encode the proteins given in
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies
 CC
 XX

SQ Sequence 1322 BP; 212 A; 417 C; 445 G; 248 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,72e-103 Length: 1322
 Score: 1694.00 Matches: 308
 Percent Similarity: 94.2% Conservative: 0
 Best Local Similarity: 94.2% Mismatches: 1
 Query Match: 98.4% Indels: 18
 DB: 10 Gaps: 1

US-09-762-577b-12 (1-309) x ACC72843 (1-1322)

QY 1 MetGlyProIleAspSerAlaIleValCysLeuHisArgGlyProGlnProSerHisTyrPala 20
 Db 174 ATGGAGACTTAAAGACAGTGCAGAGTCTGACCTGAGACCAAGCCAGCCACTGGGCA 233
 QY 21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
 Db 234 GCGGATGATGTCTCCACGACGAGCCCTGTGACCCCGCTTCTTGGCAACCTGTCTCTTA 253
 QY 41 GlyLeuAspThrCysArgAlaTyrPhePheHisValAspGlyGlnIleuGlnLeuArg 60
 Db 294 GGCCTGGAACCTGCGAGAGCTGTGGACCAAGTGAATGGGAATCTTGGGCCAGCTGGCG 353
 QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 Db 354 CCCCTGACAG 413
 QY 81 PheProGlyIleMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
 Db 414 TTCCTCGGAGATGGGCTCTGAGAGTGTGCGTCTCTCTCTATACATGGCCGTGACT 473
 QY 101 AlaGlnValProProGlnIleuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 Db 474 GCGAGAGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
 QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPheArgGlyAspAspPro 140
 Db 534 AAGGTGAGGTGCTTCTTCTGCTATGAGGAGCTGCAAGCTGGAAGCGCGGAGAGAGAG 593
 QY 141 TrpThrGlnHisAlaIleTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
 Db 594 TGGACGAGACATCCCAAGTGTCTCCCACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 653
 QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrPaspProTyr 180
 Db 654 GACTTGTTCACAGTGTCCAGAGACTCCTCCAGGCTGTGGGCTTGGAGCCCGTGG 713

OY	222	AlaGlnLeuAeArxArgIleuGIingluGuaGrThrCyAlvSvaValCysLeuAspAraArgAlaVal	242
Db	894	GCGCAAGCTCCGGCGGGCTGCAGAAGAGAGAACTGTGAAGTGTGCCCTTGACCGCGCCGTG	953
OY	243	SerIleValPheValProCysglYHHisLeuValCysAlaGlucyAlaProglYleuGln	262
Db	954	TTCATCGTCTTTGTGGCCGTGGGGCACCTGGTCTGTGCTGAATGTGGCCCCGGCTGCAG	1013
OY	263	IeuCySProIlLcYeaRgAlAProValArgSerA-gValArgThr-PheIeuSer**Ala	282
Db	1014	CTGTGCCCCCATCTGCAGAGAGCCCCCTCCGACACCCTGGCGACCTTCGTCTTAGAGCC	1072
OY	283	ArgCysHIsglVArxProglYglYleuGInserglYleuProAlaProLeuCysIleuPhe	302
Db	1074	AGGTTCACATGGCCGGCCAGAGTGGGTGCAGAGTGGACTTCCCCTGCCCCCTGTGCTGTTC	1133
OY	303	TrpThrValPheThrAlaCys	309
Db	1134	TGGACTGTGTCTGGGCTTGC	1154
RESULT 9			
AAZ61210			
ID	AAZ61210	standard; DNA; 1337 BP.	
XX	AAZ61210;		
AC	-30-MAY-2000	(first entry)	
DT			
XX		DNA encoding a human inhibitor of apoptosis protein (HIAP3).	
DE			
XX			
KW		Human; inhibitor of apoptosis protein; HIAP3; apoptosis; cancer;	
KM		chronic viral infection; neurodegenerative disorder;	
KX		chronic heart failure; dysfunctional immune response; ss.	
XX			
OS		Homo sapiens.	
FH	Key	Location/Qualifiers	
FT	CDS	/170..1066	
FT		/tag= a	
FT		/product= "human inhibitor of apoptosis protein"	
PN	MO200008144-Al.		
PD	17-FEB-2000.		
XX			
PX	23-JUL-1999;	99WO-BP005471.	
XX			
PR	31-JUL-1998;	98US-00127928.	
XX			
PA	(SCHD) SCHERING AG.		
PI	Deng G, Lin J, Morser MJ;		
DR	WPI; 2000-195573/17.		
XX	P-PSDB; AAY69182.		
PT	New DNA encoding human inhibitor-of-apoptosis protein, useful for		
PS	regulation of apoptosis.		
XX	Claim 10; Fig 1; 57pp; English.		
XX			
CC	The present sequence encodes a human inhibitor of apoptosis protein,		
CC	designated HIAP3. The protein is characterised by structural features		
CC	common to the inhibitor of apoptosis protein family. The HIAP3		
CC	polypeptides can be used for the treatment of a disease state in a human		
CC	patient, which is associated with inappropriate apoptosis and the patient		
CC	is in need of increased levels of the polypeptide. Ribozymes, which		
CC	target RNA encoding the polypeptide coding sequences, are useful for		
CC	decreasing levels of the polypeptide for treatment of inappropriate		
CC	apoptosis. Antisense nucleotide sequences are also useful for decreasing		
CC	levels of the polypeptide. Regulation of inhibitor of apoptosis proteins		
CC	may be useful in treatment of cancer, chronic viral infections,		
CC	neurodegenerative disorders, chronic heart failure and dysfunction		

CC	Immune response
XX	Sequence 1337 BP; 231 A; 413 C; 445 G; 248 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	3,76e-103
Score:	1694.00
Percent Similarity:	94.2%
Beet Local Similarity:	94.2%
Query Match:	98.4%
DB:	3
	Gaps: 1
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QY	1 MetcGlyProLyAspSerAlaYcysLeuHisargGlyProGlnProSerHisTrpAla 20
Db	170 ATGGAGCACTTAAGACAGTGCACAGTGCCTGCAACCGTGCACACACAGCCAGCACTGGGCA 229
QY	21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db	230 GCGGAGTAATGGTCCCAACGAGAGCGCTGTGACCCCGCTCTCTGGGAGAGCCCTGTCTTA 289
QY	41 GlyLeuAspTrpThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db	290 GGCCTGCAGACACTGCAGAGCCTGGGACCACTGTAGTGGGACAGATCTGGGACAGCTGGCG 349
QY	61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db	350 CCCCTGCAG 409
QY	81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
Db	410 TTCCCGGCAAGGAGCTGTGAGAGTGGCTGTGGCTCTTCCTCATGACTGGAGCCGTGACT 469
QY	101 AlaGlnValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisTrpGlnIleGlnIle 120
Db	470 GCTAGAGTGCACCCGAGCTCTGAGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 529
QY	121 LysValArgCysPhePheCysTrpGlyGlnLeuGlnSerTrpLysArgGlyAspAspPro 140
Db	530 AAGGAGAGTGTCTTCTCTGCTAGGGGCGCTGCAGAGCTGTGAAGCGGGGAGCAACCC 589
QY	141 TrpThrGlnHisAlaIleYsTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db	590 TGGACGGAGCATGCGCAAGTGGTCTCCCAAGCTGTGAGTTCCTGCTCCGGTCAAAAGAGA 649
QY	161 AspPheValHisSerValGlnGlnIleThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db	650 GACTTTGTCCACAGTGTGCAGAGAGACCTCACTCCAGCTGTGGGCTCTTGGAGACCCGTGG 709
QY	181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db	710 GAAGAACCAGAGAGCGAGCCCTGTGGCCCCCTCGCTCCGTGCTGTGGTACCTGTAG 769
QY	201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnIle----- 215
Db	770 CTGGCCCAACCCAGAGAGAGAGGTGCAGTGTGAAGTCCCGCAGAGCCAGAGAGGAGGTCA 829
QY	216 -----ProGlyAlaArgAspValGln 222
Db	830 CCAGCCAGAGCCAGAGAGGCGTGTGGTCTTGTAGCCCCCAGAGAGCGAGGATGTGGAG 889
QY	223 AlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 242
Db	890 GCGAGAGTGGGCGCGCTGCAGAGAGAGAGACGTGCAGAGGTGTGCTGTGAGCCGCGCTGG 949
QY	243 SerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGlyLeuGln 262
Db	950 TCCATCTCTTTTGGCGCGTGCAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1009
QY	263 LeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer***Ala 282
Db	1010 CTGTGCGCCCATGTGCAGAGCGCCGCTCCGAGCGCGCTGTGGCACTTCTGTCTTCAAGCC 1069

QY 283 ArgCyHISGLYArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCyLeuPhe 302
DB 1070 AGTGCATATGCGCGGCGAGTGGCTGCAGAGTGGCTCCCTCCCTCTGCTGCTTC 1129
QY 303 TTPThrValPheMetPheAlaCys 309
DB 1130 TGGACTGTGTCTTGGGCGCTGC 1150
RESULT 10
AAA15007
ID AAA15007 standard; cDNA; 1363 BP.
XX
AC AAA15007;
XX
DT 21-AUG-2000 (first entry)
XX
DE cDNA encoding a human proliferation and apoptosis related protein.
XX
KW Human; proliferation and apoptosis related protein; PROAP; psoriasis;
KW cell proliferative disorder; immunological disorder; hepatitis;
KW reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma;
KW cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia;
KW asthma; diabetes mellitus; osteoarthritis; endometriosis;
KW uterine fibroid; menstrual cycle; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 215..1111
FT /tag= a
FT /product= "proliferation and apoptosis related protein"
XX
PN WC0200023589-A2.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WC-US024511.
XX
PR 20-OCT-1998; 98US-0172216P.
PR 04-FEB-1999; 99US-0118559P.
PR 11-FEB-1999; 99US-0172229P.
PR 22-APR-1999; 99US-0154336P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Hillman JL, Guejler KJ, Corley NC, Lal P;
PI Aaimwai Y, Baughn MR, Yang J, Shih LL;
PI WPI; 2000-339688/29.
DR P-PSDB; AAY84907.
XX
PT New human proliferation and apoptosis related protein polypeptides used
PT for diagnosis, treatment and prevention of cell proliferative,
PT immunological and reproductive disorders.
XX
PS Claim 9: Page 121; 128pp; English.
XX
CC The present sequence encodes a human proliferation and apoptosis related
CC protein (PROAP). The polypeptides and polynucleotides can be used for the
CC diagnosis, treatment and prevention of cell proliferative, immunological
CC and reproductive disorders. Disorders associated with decreased
CC expression or activity of include arteriosclerosis, cirrhosis, hepatitis,
CC psoriasis, melanoma, lymphoma and cancers of the breast, brain and
CC prostate, acquired immune deficiency syndrome (AIDS), allergies, anaemia,
CC asthma, diabetes mellitus, osteoarthritis, endometriosis, uterine
CC fibroids and disruptions of the menstrual cycle. Antibodies against PROAP
CC can be used in diagnosis of disorders characterized by PROAP e.g. in ELISA
CC to detect and quantify gene expression in biopsied tissues. These
CC techniques can also be used to monitor regulation of PROAP levels during
CC therapeutic intervention
XX

SQ Sequence 1363 BP; 228 A; 428 C; 455 G; 252 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3,84E-103 Length: 1363
Score: 1694.00 Matches: 308
Percent Similarity: 94.2% Conservative: 0
Best Local Similarity: 94.2% Mismatches: 1
Query Match: 98.4% Indels: 19
DB: 3 Gaps: 1
US-09-762-577B-12 (1-309) x AAA15007 (1-1363)
QY 1 MetGlyProIleuAspSerAlaIleCysLeuHISArgGlyProGlnProSerHISTrpAla 20
DB 215 ATGGGGCTTAAAGACAGATGCGCAAGTGCCTGCACCTGTGACACACAGCCAGCCAGCTGAGCA 274
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProAspSerLeuGlySerProValLeu 40
DB 275 GCCGGTGAATGCTCCACCGACAGAGCGCTGTGACCCCGCTCTTGGAGCGCTGTCTTA 334
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 335 GGCCTGACACCTGCAGAGCGCTGGAGCACCGTGAATGGGACAGATCCTGGCCAGCTGGCG 394
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGluValAlaGlyAlaThrLeuSerArgGlyProAla 80
DB 395 CCCCTGACAG 454
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheIleArgAspTrpProLeuThr 100
DB 455 TTCCCGGCGATGGGCTTGAAGAGATGGTGTGGCTCTCTTCTATGACTGGCCGCTGACT 514
QY 101 AlaGlyValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHISGlnAsp 120
DB 515 GCTAGAGTGCACCCGAGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
QY 121 LysValArgCysPhePheCysIleGlyGlyLeuGlnSerTrpIleAspArgGlyAspAspPro 140
DB 575 AAGGAGAGTGTCTTCTTCTGCTATAGGGGCTGTGAGCTGTGAGAGCGAGAGAGAGAGAGAG 634
QY 141 TrpThrGlnHisAlaIleIleTrpPheProSerCysGlnPheLeuLeuArgSerIleGlyArg 160
DB 635 TGGACGAGAGCATGCGAAGTGTGTTCCCGAGCTGTCAAGTCTGCTGCTGCTGCTGCTGCTGCT 694
QY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlnIleSerTrpAspProTrp 180
DB 695 GACTTGTTCACAGTGTGCAGAGACTCTCACTCCAGCTGTGGCTCTTGGAGCCCGTGG 754
QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
DB 755 GAAGAAACGGAAAGCGAGCCCGCTGTGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 814
QY 201 LeuProThrProArgArgGlyValGlnSerGlnSerAlaGlnIleu----- 215
DB 815 CTGCCACACCCAGAGAGAGAGTCCAGTGTGAAGTCCAGAGAGCCAGAGAGAGGTCAGT 874
QY 216 -----ProGlyAlaArgAspValGln 222
DB 875 CCAAGCGAGGCCAGAGAGGGGTGTGGTCTTGAAGCCCGCCAGAGCCAGAGATTTGGAG 934
QY 223 AlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 942
DB 935 GCGCAGCTGGCGGCGCTGCAG 994
QY 243 SerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGlyLeuGln 262
DB 995 TCATGCTCTTGTGTGCGGCGGCGCCAGCTGTGCTGTGAGATGTGCCCCCGGCTGTGAG 1054
QY 263 LeuCyProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer***1a 282
DB 1055 CTGTGCCCATCTGCAGAGAGCCCGGTCGACCGCGTGGACCTTCTGTCTTGAAGCC 1114
QY 283 ArgCyHISGLYArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCyLeuPhe 302

Db 1115 AGGCGCATGCGCCGCGAGAGTGGGCTCCCTGCTCTGCTGTTTC 1174
 Oy 303 TrpThrValPheTrpAlaCys 309
 Db 1175 TGGACTGTGTCTGGGCTGC 1195

RESULT 11

ADT8075
 ID ADT8075 standard; cDNA; 1363 BP.

AC ADT8075;

DT 30-DEC-2004 (first entry)

XX Human proliferation and apoptosis related protein (PROAP)-18 cDNA.

KM PROAP, proliferation and apoptosis related protein;

KM cell proliferative disorder; cancer; atherosclerosis;

KM immunological disorder; AIDS; acquired immunodeficiency syndrome;

KM allergy; reproductive disorder; infertility; gene therapy; cytostatic;

KM antiatherosclerotic; immunosuppressive; anti-HIV; antiallergic;

KM antiinfertility; gynaecological; human; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 215..1111

FT /tag= a
 /product= "Proliferation and apoptosis related protein (PROAP)-18"

FT US2004203106-A1.

XX 14-OCT-2004.

XX 05-MAY-2004; 2004US-00839882.

XX 19-JAN-1999; 99US-0172216P.

PR 04-FEB-1999; 99US-0118559P.

PR 11-FEB-1999; 99US-0172229P.

PR 22-APR-1999; 99US-0154336P.

PR 19-OCT-1999; 99WO-US024511.

PR 11-APR-2001; 2001US-00807452.

XX (INCY-) INCYTE CORP.

XX Tang YT, Yue H, Hillman JL, Guegler KJ, Corley NC, Lal P;

PI Azimzai Y, Baughn MR, Yang J, Shih LL;

XX WPI; 2004-728011/71.

DR P-PSDB; ADT8056.

XX New human proliferation and apoptosis related proteins and

PT polynucleotides for diagnosing, preventing or treating disorders

PT associated with aberrant protein expression, e.g. cancer, AIDS,

PT atherosclerosis or infertility.

XX Claim 5; SEQ ID NO 37; 85pp; English.

PS The present invention relates to the human proliferation and apoptosis

XX related protein (PROAP) and its encoding nucleic acid. The invention is

CC useful for diagnosing, preventing or treating disorders associated with

CC altered expression or activity of human PROAP, such as cell proliferative

CC (e.g. cancer or atherosclerosis), immunological (e.g. acquired

CC immunodeficiency syndrome (AIDS) or allergies) or reproductive (e.g.

CC infertility) disorders. The invention is also used in screening for

CC drugs that may be used for treating or preventing the disorders mentioned

CC above and in gene therapy. The present sequence is the human PROAP-18

CC protein encoding cDNA.

XX Sequence 1363 BP; 228 A; 428 C; 455 G; 252 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:

3,84e-103

Length: 1363

Score:

1694.00

Matches: 308

Percent Similarity:

94.2%

Conservative: 0

Best Local Similarity:

94.2%

Mismatches: 1

Query Match:

98.4%

Indels: 18

DB:

13

Gaps: 1

US-09-762-577B-12 (1-309) x ADT8075 (1-1363)

Oy 1 MetGlyProLysAlaPheSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
 Db 215 ATGGGGCTTAAGACAGTGGCCAAAGTGCCTCACCTGGACACAGCGGACCACTGGGCA 274
 Oy 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 Db 275 GCGGGTATGATGTCACAGCAGAGAGCGGTGGACCCCGCTCTCGGGCAACCCCTGCTTA 334
 Oy 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlnLeuArg 60
 Db 335 GGCCTGACACCTGACAGGCTGGACCACTGGATGGGAGATCTCGGGCCACCTCGG 394
 Oy 61 ProLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
 Db 395 CCCCTGACAG 454
 Oy 81 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
 Db 455 TTCGGGCGATGGGCTCTGAGAGTGGCTGCTGGCTCTCTTATGACTGGCCGCTGACT 514
 Oy 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 Db 515 GCTGAGGTGCACCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
 Oy 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
 Db 575 AAGGTAGGTGCTTCTTCTGCTATGGGGGCTGCAGAGCTGGAAGCGGGGAGAGAGAGCC 634
 Oy 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlyPheLeuLeuArgSerLysGlyArg 160
 Db 635 TGGACGAGATGCAAGAGTGGTCCCAAGTGTCAAGTCTCTGCTCGGCTCAAGAGAGA 694
 Oy 161 AspPheValHisSerValGlnGluTrpHisSerGlnLeuLeuGlySerTrpAspProTrp 180
 Db 695 GACTTGTCCACAGTGTGCAGAGACTCACTCCCACTGCTGGGCTCTCTGGAGCCGCTGG 754
 Oy 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200
 Db 755 GAAGAACCAGAGACGAG 814
 Oy 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlu----- 215
 Db 815 CTGCCACACCCAG 874
 Oy 216 -----ProGlyAlaArgAspValGlu 222
 Db 875 CCAAGCCAGAGCCAG 934
 Oy 223 AlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 242
 Db 935 GGCACACTGGGGGCTGGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 994
 Oy 243 SerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGlyLeuGln 262
 Db 995 TCCATGTCTTGTGTGCGGCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1054
 Oy 263 LeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer***Ala 282
 Db 1055 CTGTGCCCATGTGCAG 1114
 Oy 283 ArgCysHisGlyArgProGlyGlyLeuGlnSerGlyLeuProAlaProLeuCysLeuPhe 302
 Db 1115 AGGTGCATAGCGCGGCGAG 1174

QY 303 TrpThrValPheTrpAlaCys 309
 DB 1175 TGACTGTGTCTCGGCTGC 1195
 RESULT 12
 AAL42858
 ID AAL42858 standard; DNA; 840 BP.
 AC AAL42858;
 XX
 DT 05-AUG-2002 (first entry)
 DE Survivin-like protein coding sequence 5.
 XX
 KW Survivin-like protein; diagnosis; screening; cancer; gene; ds;
 KW apoptosis abnormality; gene therapy.
 OS
 XX unidentified.
 FT Key Location/Qualifiers
 FT CDS 1..840
 FT /*tag= a
 FT /partial= a
 FT /product= "Survivin-like protein 5"
 FT /note= "No stop codon is given"
 XX
 PN MO200233071-A1.
 XX
 XX 25-APR-2002.
 XX
 XX 16-OCT-2001; 2001MO-JP009071.
 XX
 PR 17-OCT-2000; 2000JP-00316721.
 PR 20-DEC-2000; 2000JP-00386809.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Tanaka H, Kaieda I;
 XX
 DR WPI; 2002-435536/46.
 DR P-PSDB; AAO14947.
 XX
 XX Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
 PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
 PT compounds for treating various cancers and apoptosis abnormality.
 XX
 XX Disclosure; Page 122; 136pp; Japanese.
 XX
 CC The invention comprises the amino acid and coding sequences of survivin-
 CC like proteins. The survivin-like DNA and protein sequences are useful in
 CC diagnosis and screening compounds for treating various cancers and
 CC apoptosis abnormality, including gene therapy. The present DNA sequence
 CC encodes a survivin-like protein of the invention
 XX
 SQ Sequence 840 BP; 136 A; 272 C; 287 G; 144 T; 0 U; 1 Other;
 Alignment Scores:
 Pred. No.: 1,23e-93 Length: 840
 Score: 1547.00 Matches: 280
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 89.9% Indels: 0
 DB: 6 Gaps: 0
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 QY 1 MetGlyProGlyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
 DB 1 ATGGGGCCCTAAAGACAGTCCCAAGTCCCTGCACCTGTGACACACACCCAGCCACTGGGCA 60
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValIleu 40

DB 61 GCCGATGATGTCCTCCACGACGAGAGCGCTGTGACCCCGCTCTCTGGGACGCCCTGTCCAA 120
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValaAspGlyGlnIleLeuGlyValIleuArg 60
 DB 121 GGCTGGACACCTGGACAGCCTGGGACCACTGTGATGGGCANATCTGGGCCACGCTGGC 180
 QY 61 ProLeuThrGlnGluGluGluGluGluValaGlyAlaThrLeuSerArgGlyProAla 80
 DB 181 CCCCTGACAG 240
 QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
 DB 241 TTCCCGGATGGCTGTGAGAGATTGGCTCTGGCTCTCTCTTATGACTGGCGCTGACT 300
 QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 DB 301 GCTGAGGTGCCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 360
 QY 121 LysValArgCysPhePheCysTyrGlyValLeuGlnSerTrpValArgGlyAspAspPro 140
 DB 361 AAGGTAGGTGCTCTCTCTGATGGGGCCCTGCAGAGCTGAAAGCGGGAGACGACCCC 420
 QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerTyrGlyArg 160
 DB 421 TGGACGAGCATGGCCAACTGGTCCCACTGTCACTTCCCTGCTCCGTTCAAAAGAAAGA 480
 QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
 DB 481 GACTTGTTCACAGTGTGCAGAGAGACTCACTCCACGCTGTGGCTCTYGGAGACCCGTGG 540
 QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
 DB 541 GAAGAACCGGAAGACGAGCCCTGTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 600
 QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220
 DB 601 CTGCCACACCCACGAGAGAGAGTCCAGTCTGAAGTCCCGACGAGCCAGAGCCAGGAGAT 660
 QY 221 ValGluIleGlnLeuArgArgGluGlnGluGluArgThrCysLysValCysLeuAspArg 240
 DB 661 GTGAGGGCAGCTGCGCGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
 DB 721 GCCGTGTCATCGTCTTGTGCGGTGGCCACTGTCTGTCTAGTGTGCTGCTGCTGCTGCTGCTG 780
 QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 DB 781 CTGCAGCTGTGCCCATCTGCAGAGCCCGCTCCGACCGCGTGGCCACTTCTGTCTC 840
 RESULT 13
 AAF24857
 ID AAF24857 standard; cDNA; 843 BP.
 AC AAF24857;
 XX
 DT 20-APR-2001 (first entry)
 DE Nucleotide sequence of an apoptosis inhibitor designated livin.
 XX
 DE Livin, apoptosis inhibitor; IAP-3; cancer; apoptosis; gene therapy;
 KW melanoma; Alzheimer's disease; Parkinson's disease; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX FT 1..843
 XX FT /*tag= a
 XX FT /product= "livin"
 XX PN MO200077201-A1.
 PD 21-DEC-2000.

XX 09-JUN-2000; 2000WO-GB002272.
 PF 15-JUN-1999; 99US-0139291P.
 PR (ASTR) ASTRAZENCA AB.
 XX (ASTR) ASTRAZENCA UK LTD.
 PA
 PI Gomes BC, Kasof GM, Prosser JC;
 XX
 DR WPI: 2001-122843/13.
 DR P-PSDB: AAB31478.
 XX
 PT Novel livin polypeptides and polynucleotides useful for treating
 PT pathophysiological disorders related to apoptosis, cancers, particularly
 PT melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gene
 PT therapy.
 PS
 PS Claim 8; Page 54; 62pp; English.
 CC
 CC The present sequence encodes a human polypeptide, designated livin. Livin
 CC is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in
 CC certain cancer cell lines and prevents apoptosis. The livin polypeptide
 CC is useful for identifying compounds that inhibit and modulate livin
 CC function and activity. Such compounds are useful in the treatment of a
 CC dysfunctional apoptosis condition. Livin polypeptides are useful as a
 CC source of probes and primers, and in gene therapy. Livin polypeptides and
 CC polynucleotides, their inhibitors and modulators are useful for treating
 CC pathophysiological disorders related to apoptosis, cancers, particularly
 CC melanoma cancer, Alzheimer's disease and Parkinson's disease
 CC
 XX
 XX Sequence 843 BP; 138 A; 273 C; 287 G; 145 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,23e-93 Length: 843
 Score: 1547.00 Matches: 280
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 89.9% Indels: 0
 DB: 4 Gaps: 0

US-09-762-577B-12 (1-309) x AAF24857 (1-843)

QY 1 MetGlyProlysaPserAlaIyCyLeuHisArgGlyProGlnProSerHisTrpAla 20
 DB 1 ATGGAGCTTAAGACATGCGCAAGTGCCTGCACCGTGGACACCGAGCCACTGSGCA 60
 QY 21 AlAGlyAspGlyProThrGlnGluArgCyGlyProArgSerLeuGlySerProValLeu 40
 DB 61 GCCGGTATGATGTCCTCCAGCAGAGCGCTGTGACCCCGCTCTGGGCAAGCCCTGTCTTA 120
 QY 41 GlyLeuAspThrCyAsaGAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 DB 121 GGCGCTGACACCTGGACAGCCTGGAGCACGTGATGGAGATCCCTGGGCCAGCTGGCGG 180
 QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 DB 181 CCCCTGACAG 240
 QY 81 PheProGlyIleMetGlySerGlnGluLeuArgLeuAlaSerPheTyraPTrpProLeuThr 100
 DB 241 TTCCCGCGCATGGGCTCTGAGAGAGTTGCTGTGGCCCTCTTATGACTGGCGCTGACT 300
 QY 101 AlaGlyValaProProGlyIleLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 DB 301 GCTGAGGTGCAACCCGAGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 360
 QY 121 LysValaArgCyAspPhePheCyTyryGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
 DB 361 AAGGTGAGTGTCTTCTTCTGTATGGGGGCTGTGAGAGCTGGAAAGCGCGGAGAGAGAG 420
 QY 141 TrpThrGlnHisAlaIyPTrpPheProSerCyGlnPheLeuLeuArgSerLysGlyArg 160

DB 421 TGGACGAGCATGCAAGTGTTCCTCCAGCTGTCACTTCCTCGGTCCAAAGAGAGA 480
 QY AspPheValHisSerValGlnGlnIleThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
 DB 481 GACTTGTTCACAGTGTGACAGAGACTCACTCCAGCTGCTGGCTCTTGGAGCCCTGG 540
 QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyProGlu 200
 DB 541 GAAGAACCGGAGAGCGAGCCCTGTGGCCCTCGCTCCCTGCTGTGGTACCTCCAG 600
 QY 201 LeuProThrProArgArgGlnValAlaGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
 DB 601 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTCCAGAGAGAGAGAGAGAGAGAG 660
 QY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
 DB 661 GTGAGGCGGAGCTGCGCGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 241 AlaValSerIleValPheValProCyGlyHisIleLeuValCyAsaIleCyAsaAlaProGly 260
 DB 721 GCCGTGTCATCGTCTTGTGTGGCGGTGGCGGCACCTGCTGTGTGTGTGTGTGTGTGT 780
 QY 261 LeuGlnLeuCyAspProIleCyAsaGAlaProValAlaArgSerArgValArgThrPheLeuSer 280
 DB 781 CTGCAGCTGTGCCCATCTGACAGAGCCCGCTCCGAGCGCGTGGCGCACCTTCTGTCC 840
 RESULT 14
 AAS91553
 ID AAS91553 standard; cDNA; 3782 BP.
 AC
 XX AAS91553;
 DT 13-FEB-2002 (first entry)
 DE
 DE DNA encoding novel human diagnostic protein #27357.
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder; se.
 OS Homo sapiens.
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001MO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PT Drmanac RT, Liu C, Tang YT;
 PT
 DR WPI: 2001-639362/73.
 DR P-PSDB: ABG27366.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PS Claim 1; SEQ ID NO 27357; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAs64197-AAs94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC electronic format did not appear in the printed specification, but was obtained in
 CC ftp.wipo.int/pub/published_pcc_sequences

XX Sequence 3782 BP; 656 A; 1127 C; 1215 G; 716 T; 0 U; 68 Other;

Alignment Scores:

Pred. No.:	3,986-89	Length:	3782
Score:	1489.50	Matches:	282
Percent Similarity:	75.64	Conservative:	0
Best Local Similarity:	75.64	Mismatches:	3
Query Match:	86.54	Indels:	88
DB:	5	Gaps:	3

US-09-762-577B-12 (1-309) X AAs91553 (1-3782)

QY 1 MetGlyProlysaPserAlaValCysLeuHisArgGlyProGlnProSerHisTyrPala 20
 DB 2200 ATGGACCTTAAGACAGTGCACAGTGCCTGACACCTGAGACACAGCCGACCTGGGCA 2259
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 DB 2260 GCCGGTAGTGTCCACAGCAGAGAGCGCTGTGAGACCCGCTCTGGGACAGCCCTGTCTCA 2319
 QY 41 GlyLeuAspThrCysAlaGlyAlaTyrAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
 DB 2320 GGCCTGAGACACCTGACAGCCTGGACACAGTGGATGGACATCTCGGCGACGCTGGCG 2379
 QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 DB 2380 CCCTGACAG 2439
 QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
 DB 2440 TTCGCCGAGTGGGCTGTGAGAGTGGCTGTGCTGCTCTTATATACCTGGCCGCTGACT 2499
 QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThr----- 116
 DB 2500 GCTGAGGTGCCACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2559
 QY 116 ----- 116
 DB 2560 GTGTCAGACCTGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 2619
 QY 116 ----- 116
 DB 2620 AGGAGCCACGAGGCTTACAAATAGTGGACAGCCATGTCATTTGTCAGACAGTGGCT 2679
 QY 117 -----GlyHisGlnAspIleValAlaGlyCysPhePheCysTyrGlyGly 130
 DB 2680 CTGGCGGGGACCATCTGACATCAGACAGAGTGAAGTGTCTTCTTGTGCTATGAGGAGC 2739
 QY 131 LeuGlnSerTyrIleAspGlyAspAspProTyrThrGlnHisAlaIleTyrPhePro--- 149
 DB 2740 CTGCAGAGCTGGAAAGCGGGAGAGACCCCTGAGACGAGCATGCCAAGTGTGTTCCCAAG 2799
 QY 150 -----SerCysGlnPheLeuLeuArgSer 157
 DB 2800 TACCGGCTGCCCTGCGGGGCCCGGAGTCTGATTCATGCTGTCACTGCTGCTGCGGCA 2859
 QY 158 IysGlyArgAspPheValHisSerValGlnGlnIleHisSerGlnIleLeuGlySerTyr 177
 DB 2860 AAAGGAGAGACTTTGTCCACAGTGTGACAGAGACTCCCACTCCAGCTGCTGGCTCTCGG 2919

QY 178 AspProTyrGlnGlnProGlnLeuAspAlaAlaProValAlaProSerValProAlaSerGly 197
 DB 2920 GACCCCTGGGAAAGAACCGGAGAGCGACGCCCTGTGGCCCTCC-----GCA 2964
 QY 198 TyrProGlnLeuProThrProArgHisGlnValGlnSerGlnSerAlaGlnGlnProGly 217
 DB 2965 ----- 2965
 QY 218 AlaArgAspValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 237
 DB 2968 GCCAGGAGTGTGAGAGCGGACGCTGCGCGCGCTGACAGAGAGAGACCGTGCAGAGTGTGC 3027
 QY 238 LeuAspArgAlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCys 257
 DB 3028 CTGACCGCGCGCGTGTCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3087
 QY 258 AlaProGlyLeuGlnLeuGlnCysProIleCysArgAlaProValArgSerArgValArgThr 277
 DB 3088 GCCCGCGGCTGCACACTGTGCCCCCATCTGACAGAGCCCGCTCCGACGCGGTGGCACCC 3147
 QY 278 PheLeuSer***AlaArgCysHisGlyArg-ProGlyGlyLeuGlnSerGlyLeuProAl 297
 DB 3148 TTCTGTCTCTAGGCGCAGTGGCCATGCGCGCGGTGGGTGGCTGACAGTGGGCTCTCCG 3207
 QY 297 aProLeuCysLeuPheTyrThrValPheTyrAlaCys 309
 DB 3208 CCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3244
 RESULT 15
 AAD16365 standard; DNA; 769 BP.
 ID AAD16365;
 AC AAD16365;
 XX 19-NOV-2001 (first entry)
 DT
 DE Human SBH80014.1Aa gene #2.
 KW Human; Alzheimer's disease; amyotrophic lateral sclerosis; ALS;
 KW Zöllinger-Ellison syndrome; immune system disease; echinophrenia;
 KW inflammation; haematopoietic disease; anxiety; feeding disorder; aging;
 KW anorexia; depression; cardiovascular disease; sleep disorder; seizure;
 KW memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia;
 KW sexual disorder; growth abnormality; infection; autoimmune disease;
 KW rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis;
 KW cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease;
 KW hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity;
 KW diabetes mellitus; glomerulonephritis; renovascular hypertension; cancer;
 KW vaccine; gene therapy; SBH80014.1Aa gene; ds.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT 1..768
 FT /*tag= a
 FT /product= "Human SBH80014.1Aa protein #2"
 FT /transl_except= (pos:688..696, aa:Cys-Val)
 FT /note= "CDS does not include stop codon"
 FT /partial
 XX
 PN MO200160850-A1.
 XX
 PD 23-AUG-2001.
 XX
 PF 14-FEB-2001; 2001MO-US004703.
 XX
 PR 14-FEB-2000; 2000US-0182172P.
 PR 29-FEB-2000; 2000US-0186084P.
 PR 18-APR-2000; 2000US-0198583P.
 PR 04-OCT-2000; 2000US-0237963P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Kabnick KS, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
 XX WPI: 2001-536566/59.
 DR P-PSDB: AAB09458.
 XX
 PT New secreted and membrane associated polypeptides for treating
 PT Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
 PT disorders, stroke, and asthma.
 XX

PS Claim 2; Page 53; 94pp; English.

XX The present sequence is a gene encoding human SBH80014.IAPA protein, a
 CC cytosolic protein of the invention. The invention relates to secreted and
 CC membrane associated polypeptides and nucleic acid molecules encoding such
 CC polypeptides. Sequences of the invention are useful for treating diseases
 CC such as Alzheimer's disease, amyotrophic lateral sclerosis (ALS),
 CC Zöllinger-Ellison syndrome, diseases of the immune system, haematopoietic
 CC disease, inflammation, anxiety, schizophrenia, feeding disorders,
 CC anorexia, depression, social, sexual and rewarded behaviour,
 CC cardiovascular disease, sleep disorder, learning and memory alteration
 CC and altered immune response, seizure, migraine, cancer, stroke, asthma,
 CC neuropathy, aging, sexual disorders, treatment of transexuals, growth
 CC abnormalities, obesity, infections, autoimmune diseases (e.g. Rheumatoid
 CC arthritis), cataractogenesis, angiogenesis, disorders associated with
 CC healthy maintenance of gastric mucosa and repair of acute and chronic
 CC mucosal lesion, lung carcinoma, cerebral ischemia, atherosclerosis,
 CC cirrhosis, Huntington's disease, headache, amnesia, multiple sclerosis,
 CC Hodgson's disease, dilated cardiomyopathy, congestive heart failure,
 CC cardiac arrhythmias, hypercholesterolemia, viral and non-viral
 CC hepatitis, type I and type II diabetes mellitus, glomerulonephritis,
 CC renovascular hypertension, hypoglycaemia, periodic paralysis, tendinitis
 CC and malignant hyperthermia. Polypeptides of the invention are used to
 CC identify membrane bound and soluble receptors. They are also useful as
 CC vaccines for inducing an immunological response in a mammal.
 CC Polynucleotides of the invention are used in gene therapy. They are also
 CC valuable for chromosome localisation studies and tissue expression
 CC studies
 XX

XX Sequence 769 BP; 122 A; 248 C; 265 G; 134 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,99e-82 Length: 769
 Score: 1372.50 Matches: 255
 Percent Similarity: 91.1% Conservative: 0
 Best Local Similarity: 91.1% Mismatches: 1
 Query Match: 79.8% Indels: 25
 DB: 4 Gaps: 1

US-09-762-577b-12 (1-309) x AAD16365 (1-769)

QY 1 MetGlyProLysAspSerAlaValCysLeuHisArgGlyProGlnProSerHisTrpAla 20
 DB 1 ATGGGACCTTAAAGAGTGCACAGTGCCTCACCCTGGACACAGCCGACCTGGGCA 60
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 DB 61 GCCGGATGATGCTCCACGCGAGAGCGCTGTGAGACCCGCTCTCGGGCAGCCCTGTCCTA 120
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 DB 121 GGCCTGGACACCTGGAGAGCTGGACACCACTGGATGGGCAATCCCTGGGCGAGCTGG 180
 QY 61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
 DB 181 CCTCTACAG 240
 QY 81 PheProGlyMetGlySerGlyGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
 DB 241 TTCCCGGCGATGGGCTGTGAGAGTGGCTGTGGCTCTTCTATGACTGGCGGCTGACT 300
 QY 101 AlaGluValProProGlyLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120

DB 301 GCTGAGGTGCCACCCGAGCTGTGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGAGAC 360
 QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
 DB 361 AAGGTAGAGTGTCTTCTGTCTATGGGGGCTGTCAAGGCTGGAAAGCCGGGGAGACGCC 420
 QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlyPheLeuLeuArgSerLysGlyArg 160
 DB 421 TGGACCGAGCATCCCAAGTGTCCCC--TGTCAGTCTCTGCTCCGCTCAAAAGAGAGA 478
 QY 161 AspPheValHisSerValGlnGluTrpHisSerGlnLeuLeuGlySerTrpAspProTrp 180
 DB 479 GACTTGTCCACAGTGTGCGAGAGACTCACTCCACAGTGTGGGCTCTGGACCCGTTGG 538
 QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
 DB 539 GAAGAAACCGAAGACGACGACCTGTGGCCCTCC----- 574
 QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220
 DB 575 -----GGAGCCAGGAT 586
 QY 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGluArgTrpCysLysValCysLeuAspArg 240
 DB 587 GTGAGAGCCAGCTGCGCGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 646
 QY 241 AlaValSerTleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
 DB 647 GCGGTTCATCGTCTTTGTGCGGTGCGGCACACTGTGTGTAGTGTGCCCGCGGC 706
 QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgTrpPheLeuSer 280
 DB 707 CTCACACTGTCCCATCTGCAGAGCCCGCTCCGAGCGCGCTGGCACCTTCTGTTC 766

Search completed: April 19, 2006, 23:48:47
 Job time : 691 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2006, 20:00:00 ; Search time 4510 Seconds
(without alignments)
3205.589 Million cell updates/sec

Title: US-09-762-577B-12

Perfect score: 1721

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Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Total number of hits satisfying chosen parameters: 82156650

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_esc2:*
3: gb_esc3:*
4: gb_hc:*
5: gb_esc4:*
6: gb_esc5:*
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9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	76.1	924	5	BQ682827 AGENCOURT
2	1270	73.8	884	5	BUI95879 AGENCOURT
3	1252.5	72.8	808	2	BG761924 602718156
4	1252	72.7	797	2	BG766472 602739233
5	1246	72.4	843	11	DD053047 Homo sapi
6	1235.5	71.8	877	2	BG770075 602745008
7	1206	70.1	982	5	BQ682897 AGENCOURT

Result No.	Score	Query Match	Length	DB ID	Description
8	1194	69.4	912	5	BQ682378 AGENCOURT
9	1194	69.4	929	5	BQ892691 AGENCOURT
10	1189	69.1	655	2	BG760550 602716990
11	1187.5	69.0	849	2	BG760865 602717048
12	1187	69.0	870	5	BQ877438 AGENCOURT
13	1172	68.1	945	5	BUI80020 AGENCOURT
14	1156	67.2	891	6	CD051153 AGENCOURT
15	1153.5	67.0	919	5	BQ877652 AGENCOURT
16	1153	67.0	621	6	CD673774 604c01.Y
17	1145	66.5	956	5	BUI72109 AGENCOURT
18	1137	66.1	920	5	BQ676590 AGENCOURT
19	1136	66.0	740	2	BG768992 602742920
20	1131.5	65.7	918	5	BUI50825 AGENCOURT
21	1129	65.6	902	5	BUI83453 AGENCOURT
22	1082	62.9	830	2	BG762467 602733911
23	1074.5	62.4	824	2	BG770578 602734106
24	1074.5	62.4	956	5	BUI68025 AGENCOURT
25	1071	62.2	994	2	BF690534 602187029
26	1069.5	62.1	958	5	BUI88703 AGENCOURT
27	1060	61.6	842	2	BG770473 602734384
28	1046.5	60.8	579	6	CD673799 604g07.Y
29	1044	60.7	616	2	BG767481 602741287
30	1026	59.6	603	3	BW696272 UI-B-DW0-
31	1015.5	59.0	843	2	BG766949 602740652
32	981	57.0	555	2	BF726384 by05h02.Y
33	973	56.5	741	2	BG763960 602736948
34	961.5	55.9	905	5	BUI63067 AGENCOURT
35	931	54.1	769	6	CD743169 UI-H-FT1-
36	913	53.1	1531	4	AK053463 Mus muscu
37	903	52.5	652	2	BG763730 602735757
38	895.5	52.0	967	2	BF690431 602186881
39	893.5	51.9	952	5	BQ678815 AGENCOURT
40	865.5	50.3	623	3	BM700577 UI-B-DW1-
41	858	49.9	968	5	BQ679311 AGENCOURT
42	850.5	49.4	872	5	BQ878898 AGENCOURT
43	849	49.3	827	8	DN867848 na330d08.
44	843	49.0	665	3	BM704611 UI-B-C11-
45	835	48.5	553	2	BF689631 602187029

ALIGNMENTS

RESULT 1
BQ682827 924 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT_8507903 NIH_MGC_112 Homo sapiens CDNA clone IMAGE:6294748
DEFINITION 5', mRNA sequence.
ACCESSION BQ682827
VERSION BQ682827.1 GI:21795506
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGNANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 924)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strauberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LICM2499 row: 0 column: 05
High quality sequence stop: 673.
Location/Qualifiers
1. 924
/organism="Homo sapiens"

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/mol_type="mRNA"
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/notes="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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ORIGIN

Alignment Scores:

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Pred. No.: 1 43e-97 Length: 924
Score: 1310.00 Matches: 254
Percent Similarity: 89.2% Conservative: 3
Best Local Similarity: 88.2% Mismatches: 6
Query Match: 76.1% Indels: 25
DB: 5 Gaps: 5

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US-09-762-577B-12 (1-309) x B0682827 (1-924)

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OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
DB 64 ATGGGACCTAAAGACAGTGGCCAGTGGCTGCACCTGGACCAACAGCCGAGCCACTGGGCA 123
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 124 GCGGTGTGTGTCCTCCACGACGAGGAGCTGTGACCCCGCTCTGGGACAGCCCTGCTCTA 183
OY 41 GlyLeuAspTyrCysArgAlaTyrAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
DB 184 GGCCTGGACACCTCGAGAGCCTGGGACCACTGATGGGACAGATCTGGGCGACCTGGG 243
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 244 CCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
OY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAspSerPheTyrAspTyrProLeuThr 100
DB 304 TTCCCGGCGATGGGCTCTGAGAGATGTGTGCTTCCTCTTAATGACTGGCGCTGACT 363
OY 101 AlaGlyValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 364 GCTGAGGTGGCCACCCGAGCTGTGGCTGTGGCTTTCTTCCACACAGGCATCGAGAC 423
OY 121 LysValArgCysPhePhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140
DB 424 AAGGTGAGTGTCTTCTCTGTATGGGGGCTGTGACAGCTGAAAGCGGGGAGACGCC 483
OY 141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 484 TGGACGAGATGATGCAAGTGTCTCCCAAGCTGATGTTCTGTCTCCGGTCAAAAAGAGAA 543
OY 161 AspPheValHisSerValGlnGlnTyrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
DB 544 GACTTGTCTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGCTCTCTGGACCCGTGG 603
OY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200
DB 604 GAAGAAACCGGAAAGACGAGCCCTGTGGCCCTCCGTCTCTGTGGTACCTGTGAG 663
OY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGln----- 215
DB 664 CTGCCCCACACCCAGAGAGAGAGTCCAGTCTGAAGTGTCCAGAGAGCCAGAGAGGCTCA 723
OY 216 -----ProGlyAlaArgAspValGln 222
DB 724 CAGCCGAGGCCCCAGAGGGCGTGTGGTCTTGAAGCCCCAGAGAGCCAGGAGTGTGGAA 783

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OY 223 -AlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 241
DB 784 GGCCACACTCGGGCGCTGACAGAGAGAGAGACTGCTCAAGTGTCCCTGGAGCGGCGCC 843
OY 242 -ValSerIle---ValPheValProCys-GlyHis-Leu---ValCysAlaGlnCysAla 258
DB 844 GTGTGTCATGGGCTTTTGTGGCGCTGTGGCGCCACCTGTGGTGTGCTGATGTGTGCC 903
OY 259 Pro---GlyLeuGlnLeu 263
DB 904 CCCCCGGGCTTCGCACTT 921

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RESULT 2

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BUI95879 884 bp mRNA linear EST 04-SRP-2002
LOCUS LOCUS
DEFINITION AGENCOURT 8050326 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089315
5', mRNA sequence.
ACCESSION BUI95879
VERSION BUI95879.1 GI:22709863
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 884)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LINC2328 row: O column: 12
High quality sequence steps: 658.
Location/Qualifiers
1..884
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/notes="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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FEATURES

source

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1..884
/organism="Homo sapiens"
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/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/notes="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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ORIGIN

Alignment Scores:

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Pred. No.: 2 67e-94 Length: 884
Score: 1270.00 Matches: 245
Percent Similarity: 89.5% Conservative: 1
Best Local Similarity: 89.1% Mismatches: 7
Query Match: 73.8% Indels: 22
DB: 5 Gaps: 1

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US-09-762-577B-12 (1-309) x BUI95879 (1-884)

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OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
DB 64 ATGGGACCTAAAGACAGTGGCCAGTGGCTGCACCTGGACCAACAGCCGAGCCACTGGGCA 123

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[illegible][illegible]

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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
--DNA Sequencing by: Incyte Genomics, Inc.
--clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: LLCM1674 row: P column: 13
High quality sequence stop: 806.
location/Qualifiers
1..808
source

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/organism="Homo sapiens"
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/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_1b="N1H_MGC_49"
/note="Organ: skin; Vector: pOT81; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a N1H_MGC
Library. |"

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[illegible]

Qy	3	ProLysAspSerAlaIysCysLeuNhiIaRgIyProGlnProSerNhiIaSTPAlaIaGly	22
Db	2	CGTAAAGACAGTGCAGATGGCTGGACCTGGACCAAGCCGACCACTGGGACGCCGT	61
Qy	23	AapGlyProThrGlnGluArgCysGlyProArGSerLeuGlySerProValLeuGlyLeu	42
Db	62	GATGGTCCACGACGAGACGGCTGTGGACCCCGCTCTGTGGACACCTGTCTTAAAGCTTG	122
Qy	43	AapThrCysArgAlaTrp-AspNhiIsvaIAsp-GlyGlnIleLeu-GlyGlnLeuArg-Pr	61
Db	122	GACACTGTGAGAGCTGTGGACCAAGTGGATGTGGAGATCTGTGGCCAGCTCTGGCC	181
Qy	61	OleuThrGluGluGluGluGluGlu-GlyAla-GlyAlaThrIleuSerArg-GlyProAl	80
Db	182	CCTGCACAGGGAGGAAAGAGAGAGTGGCGCTGGGGCCACTTGTCTCAGGGTGGCTGC	241
Qy	80	AapHeProGlyIweGlySerGluGluLeuArgLeuAlaSerPheThrAspTrpProLeuTh	100
Db	242	CTTCCCCCGCATGGGCTCTGAGAGATGGCGTCTGGCTCTCTATATACCTGGCCGGCTGAC	301
Qy	100	rAlaGluValProProGluLeuLeuAlaAlaIaGlyPhePheNhiIaThrGlyNhiIaGlnAs	120
Db	302	TGCTAGAGGTGCACCCGAGCTGTGGCTGTGGCGGGCTTCTTCCACACAGGCCATCAGGA	361
Qy	120	PlyValAlaArgCysPhePheCysIlyrGlyGlyIleuGlnSerTrpIysArgIysAspAspPr	140
Db	362	CAAAGGTGAGGGCTTCTTCTGCTATGGGGGCTGGACAGCTGGAAAGGCCGGAGACCACCC	421
Qy	140	OTrpThrGluNhiIaAlaIySTrPheProSerCysGlnPheLeuLeuArgSerIysGlyAr	160
Db	422	CTGGACGGAGCATGCCAAGTGCTTCCCAAGCTGTCAATTCCTGTCTCCGGTCAAAAGGAAG	481
Qy	160	GAsPheValNhiIaSerValGlnGluThrNhiIaSerGlnLeuLeuGlyIysTrpAspProTr	180
Db	482	AACATTTTGTCCACAGTGTGACGAGAGACTTCACTCCCACTGTCTGGGCTCTCGGAGACCCGG	541

Hubisz, M.J., Friedel-Alon, A., Tanenbaum, D.M., Civeello, D., White, T.J., Sinsky, J.J., Adams, M.D. and Cargill, M. A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
 JOURNAL PUBLISHED (et) PLOS Biol. 3 (6), E170 (2005)
 REFERENCE 15869325
 AUTHORS 2 (bases 1 to 843)
 TITLE Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Friedel-Alon, A., Tanenbaum, D.M., Civeello, D., White, T.J., Sinsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
 JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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ORIGIN
 Alignment Scores:
 Pred. No.: 2,38e-92 Length: 843
 Score: 1246.00 Matches: 237
 Percent Similarity: 84.6% Conservative: 0
 Best Local Similarity: 84.6% Mismatches: 43
 Query Match: 72.4% Indels: 0
 DB: 11 Gaps: 0

US-09-762-577B-12 (1-309) x DQ053047 (1-843)

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QY 1 MetGlyProLyAspSerAlaLyScyLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGGACCTAAAGACAGTCCCAAGTCCCTGCACCGTGACCAACAGCCGAGCCATGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGlnuArgCyGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCGGTGATGTCTCCACGACGAGCGCTGTGAGACCCCGCTCTGTGGGACGCCCTGTCTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
DB 121 GGCCTGGACCTCGACAGACCTGGGACCACTGGAATGGGACATCTCGGCGCACGCTGCG 180
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 241 TTCCCGCGCATGTGGCTCTGAGAGAGTTGGCTGTGGCTCTTATGACTGCGCGCTGACT 300
QY 101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GGTGAGGTGCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 360
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLyAspGlyAspAspPro 140
DB 361 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 420
QY 141 TrpTrpGlnHisAlaLysTrpPheProSerCysGlnPheLeuArgSerIysGlyArg 160
DB 421 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480
QY 161 AspPheValHisSerValGlnGlnTrpHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 481 GACCTTGTCACAGTGTGACGAGACTCATCCACAGCTGTGGGCTCTTGGAGACCCGAG 540
  
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QY 181 GlnGlnProGlnuAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200
 DB 541 GAAAGACCGGAAGANN 600
 QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlnValaArgAsp 220
 DB 601 CTGCCACACCCAGAT 660
 QY 221 ValGlnValGlnLeuArgArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
 DB 661 GTGAGAGGCGAGCTCGGCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
 DB 721 GCGGTGTCATGTGTCTTGTGTGCGCGCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 QY 261 LeuGlnLeuCybProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 DB 781 CTGACAGTGTGCCCATCTGACAGAGCCCGCGCCAGCCGCGTGCACCTTCTGTCTTC 840

RESULT 6
 LOCUS BG770075 877 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602745008P1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4878193 5', mRNA sequence.
 ACCESSION BG770075
 VERSION BG770075.1 GI:14080728
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo
 1 (bases 1 to 877)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: L1CML1763 row: P column: 02
 High quality sequence stop: 819.

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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ORIGIN
 Alignment Scores:
 Pred. No.: 1.84e-91 Length: 877
 Score: 1235.50 Matches: 246
 Percent Similarity: 89.2% Conservative: 2
 Best Local Similarity: 88.5% Mismatches: 9

Query Match: 71.8% Indels: 24
DB: 2 Gaps: 2
US-09-762-577B-12 (1-309) x BG770075 (1-877)

QY 1 MetGlyProlyAspSerAlaValGlyLeuHisArgGlyProGlnProSerHisTTPAla 20
DB 55 ATGGAGACTTAAGAAGAGAGTGGCAAGTGGCTGGACCCCTGGACCAAGCCGAGCCACTGGACA 114

QY 21 AlaGlyAspGlyProThrGlnGluArgGlyProArgSerLeuGlySerProValLeu 40
DB 115 GCGGATGATGATCCACGACGAGAGCCGTGTGAGACCCCGCTCTGTGGACGCTGTCTTA 174

QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 175 GGCCTGGACACCTGGACAGCTGGACCAAGTGAATGGCAATCTCTGGGAGAGCTGGCG 234

QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGln 80
DB 235 CCGCTGACAG 294

QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTTPProLeuThr 100
DB 295 TTCCTGGCATGGGCTCTGAGAGATGGCTGTGGCTCTCTTATGACTGGCCCTGACT 354

QY 101 AlaGlnValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 355 GCTGAGGTGCACCCAGAGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 414

QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnIleLeuGlnIleLeuGlyAspAspPro 140
DB 415 AAGGTAGGTGCT 474

QY 141 TTPThrGlnHisAlaValTTPPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 475 TGGACGAGACATGGCCAAAGTGTCTCCAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 534

QY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTTPAspProTTP 180
DB 535 GACTTGTTCACAGTGTGCAGAGAGACTCACTCCAGCTGTGGCTGTGGCTGTGGCTGTGG 594

QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 595 GAAGAAGCCGAG 653

QY 201 LeuPro-ThrProArgArgGlnValGlnSerGlnSerAla----- 213
DB 654 CTGCCACACC--AGGAGAGAGGTCCAGTCTGAAGTGCACAGAGCCAGAGAGAGAGTCACT 710

QY 214 -----GlnGluProGlyAlaArgAspValG 222
DB 711 CCAGCCGAGGCGCAGAGGCGGTGTGGGCTCTTGGAGCCCGCCAGAGAGCCAGGAGATGG 770

QY 222 LuAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 242
DB 771 AGGCGCACTTGGCGGCTGCAG 830

QY 242 alSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAla 258
DB 831 G-TCTTGTCTTGT 877

RESULT 7
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LOCUS AGENCOURT 8210542 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6259145
DEFINITION B0682897 B0682897.1 GI:21795576
ACCESSION B0682897
VERSION B0682897.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 982)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2416 row: c column: 18
High quality sequence stop: 623.
Location/Qualifiers
1..982
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6259145"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGACGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 5,85e-89 Length: 982
Score: 1206.00 Matches: 216
Percent Similarity: 99.5% Conservative: 0
Best Local Similarity: 99.5% Mismatches: 1
Query Match: 70.1% Indels: 0
DB: 5 Gaps: 0

US-09-762-577B-12 (1-309) x B0682897 (1-982)

QY 1 MetGlyProlyAspSerAlaValGlyLeuHisArgGlyProGlnProSerHisTTPAla 20
DB 64 ATGGAGACTTAAGAAGAGAGTGGCAAGTGGCTGGACCCCTGGACCAAGCCGAGCCACTGGACA 123

QY 21 AlaGlyAspGlyProThrGlnGluArgGlyProArgSerLeuGlySerProValLeu 40
DB 124 GCGGATGATGATCCACGACGAG 183

QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 184 GGCCTGGACACCTGGACAGCTGGACCAAGTGAATGGCAATCTCTGGGAGAGCTGGCG 243

QY 61 ProLeuThrGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 244 CCGCTGACAG 303

QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTTPProLeuThr 100
DB 304 TTCCTGGCATGGGCTCTGAGAGATGGCTGTGGCTCTCTTATGACTGGCCGCTGACT 363

QY 101 AlaGlnValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 364 GCTGAGGTGCACCCAGAGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 423

QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnIleLeuGlnIleLeuGlyAspAspPro 140
DB 424 AAGGTAGGTGCT 483

QY 141 TTTpThrGluHieAlaIalysTrpPheProSerCysGlnPheLeuLeuArgSerIysGlyArg 160
 DB 484 TGGACGAGCATGATCCCAAGTGGTTCCTCCAGCTTCCTGCTCCGCTCAAAAGGAGAGA 543
 QY 161 AAPPheValHieSerValGlnGlnThrHieSerGlnLeuLeuGlySerTrpAspProTrp 180
 DB 544 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGACTCTGGGCTCTGGGAGCCCGTGG 603
 QY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200
 DB 604 GAAGAACCAGAGACGACGACCCCTGTGGCCCTCCCTCCCTCTGAGTACCTTGAG 663
 QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
 DB 664 CTGCCACACACCCAGAGAGAGGTCCAGTCTGGAGAGTCCAGAGAGCCAGAGA 714

RESULT 8
 B0682378 912 bp mRNA linear EST 15-JUL-2002
 LOCUS B0682378
 DEFINITION AGENCOURT 8185884 NIH_MGC_112 Homo sapiens CDNA clone IMAGE:6263255
 5', mRNA sequence.
 ACCESSION B0682378
 VERSION B0682378.1 GI:21795057
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 912)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2426 row: n column: 24
 High quality sequence stop: 609.
 Location/Qualifiers

FEATURES
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 1..912
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6263255"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_11b="NIH_MGC_112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 5.15e-88 Length: 912
 Score: 1194.00 Matches: 215
 Percent Similarity: 99.5% Conservative: 0
 Best Local Similarity: 99.5% Mismatches: 1
 Query Match: 69.4% Indels: 0
 DB: 5 Gaps: 0

US-09-762-577B-12 (1-309) x B0682378 (1-912)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHieIArgGlyProGlnProSerHieIstPAla 20
 DB 64 ATGGACCTTAAAGACAGTGGCCAGTGGCTGACCGTGGACCAACAGCCAGGACCTGGGA 123
 QY 21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProAspSerLeuGlySerProValLeu 40
 DB 124 GCCGGTGTATGGTCCACACAGAGAGCGCTGTGACCCCTCTCTGGGAGCCCTGTCTTA 183
 QY 41 GlyLeuAspThrCysArgAlaIstPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 DB 184 GGCCTGGACACTGACAGAGCTGGGACCACTGAGTGGAGCAATCTGAGCTGAGCTGGCG 243
 QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGlu 80
 DB 244 CCCCTGACAG 303
 QY 81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
 DB 304 TTCCCGGCGCATGGGCTGTGAGAGATTGGCTGGCTCTCTTATGACTGGCCGCTGACT 363
 QY 101 AlaGluValProProGlnLeuLeuAlaAlaIstPhePheHieThrGlyHieGlnAsp 120
 DB 364 GCTGAGTGGCCACCCGAGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGT 423
 QY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
 DB 424 AAGTGAAGTGTCTTCTTCTGCTTGGGGCTGTGACAGCTGGAAGCGGGAGACACCC 483
 QY 141 TTTpThrGluHieAlaIalysTrpPheProSerCysGlnPheLeuLeuArgSerIysGlyArg 160
 DB 484 TGGACGAGCATGACCAAGTGGTTCCTCCAGCTGTCAGTTCCTGCTCCGCTCAAAAGGAGA 543
 QY 161 AAPPheValHieSerValGlnGlnThrHieSerGlnLeuLeuGlySerTrpAspProTrp 180
 DB 544 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGACTCTGGGCTCTGAGACCCGTGG 603
 QY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200
 DB 604 GAAGAACCAGAGACGACGACCCCTGTGGCCCTCCCTCCCTCTGAGTACCTTGAG 663
 QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 216
 DB 664 CTGCCACACACCCAGAGAGAGGTCCAGTCTAAAGTGGCCAGAGAGCC 711

RESULT 9
 B0892691 929 bp mRNA linear EST 16-AUG-2002
 LOCUS B0892691
 DEFINITION AGENCOURT 8095843 NIH_MGC_112 Homo sapiens CDNA clone IMAGE:6087832
 5', mRNA sequence.
 ACCESSION B0892691
 VERSION B0892691.1 GI:22284705
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 929)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2325 row: a column: 17
 High quality sequence stop: 628.
 Location/Qualifiers

FEATURES

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1. .929
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/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI, Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 5.28e-88 Length: 929
Score: 1194.00 Matches: 220
Percent Similarity: 96.1% Conservative: 1
Best Local Similarity: 95.7% Mismatches: 6
Query Match: 69.4% Indels: 3
DB: Gaps: 1

US-09-762-577B-12 (1-309) x BQ892691 (1-929)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTTPAla 20
Db 90 ATGGGACCTTAAGACAGTCCCAAGTCTGACACCGTGACACACCGACCGACCTGGGCA 149
QY 21 AAlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 150 GCGGGTGAATGTCCTCCACGACGAGCGCTGTGACCCCGCTCTGGGACGCTCTCTTA 209
QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 210 GGCCTGGACACTGACAGACCTGGAGACCACTGAGTGGAGATCTTGGGACACTGGCG 269
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 270 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 329
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 330 TTCCCGGCGATGGGCTCTGAGGAGTTCGCTGCGCTCTCTCTATGACTGCGCGTACT 389
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlnHisGlnAsp 120
Db 390 GGTGAGGTGGCCACCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 449
QY 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTTPAspArgGlyAspAspPro 140
Db 450 AAGGTGAGGTGCTTCTTCTGCTATGGGGGCTTGGAGAGCTGGAGAGAGAGAGAGAGAG 509
QY 141 TrpThrGlnHisAlaLysTTPAspPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
Db 510 TGGACGGAGCATGCTCAAGTGTGCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db 570 GACCTTGTCCACAGTGGACGAGAGACTCACTCCAGCTGCTGCTGCTGCTGCTGCTGCTG 629
QY 181 GlnGlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200
Db 630 GAAAGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnPro-----GlyAl 218
Db 690 CTGCCACACCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 749
QY 218 ArgArgPheValGlnAlaGlnLeuArgArg 227
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Db 750 GTTCACGCCGAGGCCCAAGAGGCGCT 777
RESULT 10 655 bp mRNA linear EST 15-MAY-2001
Bg760550
LOCUS 602716990F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4840294 5',
DEFINITION mRNA sequence.
ACCESSION Bg760550.1 GI:14071203
VERSION Bg760550
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 655)
NIH-MGC http://img.cni.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabds-remail.nih.gov
Tissue Procurement: ATCC/CDT/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1671 row: d column: 23
High quality sequence stop: 655.
Location/Qualifiers
1. 655
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/clone="IMAGE:4840294"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH MGC 49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI, Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
library."

ORIGIN

Alignment Scores:
Pred. No.: 8.34e-88 Length: 655
Score: 1189.00 Matches: 217
Percent Similarity: 99.5% Conservative: 0
Best Local Similarity: 99.5% Mismatches: 1
Query Match: 69.1% Indels: 1
DB: Gaps: 0

US-09-762-577B-12 (1-309) x Bg760550 (1-655)

QY 3 ProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTTPAlaAlaGly 22
Db 2 CCTAAAGACAGTGGCCAAAGTCTGACACCGTGGACACGCGGACCTGGGAGCGCGGT 61
QY 23 AspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 42
Db 62 GATGTCTCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
QY 43 AspThrCysArgAlaTTPAspHisValAspGlyGlnLeuGlnGlnGlnGlnGlnGlnGln 62
Db 122 GACACCTGCAAGAGCTTGGAGACCACTGAGATGGAGATCTTGGAGCAGCTGCGGCGCTG 181
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5', mRNA sequence.
 ACCESSION B0877438
 VERSION B0877438.1 GI:22269446
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 870)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (ULNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
 Plate: LNCM231 row: e column: 07
 High quality sequence stop: 580.

FEATURES
 source
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6090222"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1,82e-87 Length: 870
 Score: 1187.00 Matches: 216
 Percent Similarity: 99.1% Conservative: 0
 Best Local Similarity: 99.1% Mismatches: 1
 Query Match: 69.0% Indels: 1
 DB: 5 Gaps: 0

US-09-762-577b-12 (1-309) x B0877438 (1-870)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
 Db 64 ATGGACCTTAAGACAGTGCCTGACCGTGGACCAACGCCGACCTGGGCA 123
 QY 21 AlaGlyAspGlyProThrGlnGlnGlyArgGlyProArgSerLeuGlySerProValLeu 40
 Db 124 GCCCGTAGTGTCCACGACGAGAGCGCTGTGGACCCGCTCTTGGGCGACCCCTGCTTA 183
 QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnIleuArg 60
 Db 184 GGCTTGACACCTGACAGGCTGGGACCACTGATGGGAGATCTTGGGCGACGCTGGCG 243
 QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 Db 244 CCCCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 303
 QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
 Db 304 TTCCCGGCACTGGGCTGTGAGAGATTGCGTGGCTCTTCTATGACTGGCGGCTGACT 363

QY 101 AlaGlnValProProGlnIleLeuAlaAlaGlyPhePheHisTyrGlyHisGlnAsp 120
 Db 364 GCTAGGTGGCCACCGGAGCTGCTGGCTGGCGGCTTCTTCCACACAGGCACTGAGAC 423
 QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPheArgGlyAspAspPro 140
 Db 424 AAGGTAGGTGCTCTTCTTCTGCTATGGAGGCTGAGAGTGGAGAGCGGGGAGGACCC 483
 QY 141 TyrThrGlnHisAlaIleTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
 Db 484 TGGACGAGGATCGCAAGTGTGTCACAGCTGTCCAGTCTCCGGTCAAAAGAGAGA 543
 QY 161 AspPheValHisSerValGlnGlnIleThrHisSerGlnIleLeuGlnGlySerTyrAspPro 180
 Db 544 GACTTGTCCACAGTGTGACGAGAGCTCACTCCACTGTGGGCTCTGNGACCCGCTGG 603
 QY 181 GlnGlnProGlnAspAlaAlaProVal-AlaProSerValProAlaSerGlyTyrProGly 200
 Db 604 GAAGAACCGGAAACGAGGCGCTGTGGGCGCCCTCCGTCCTGCTGTGGTACCTTGA 663
 QY 200 UleuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGly 217
 Db 664 GTGCCCAACCCAGAGAGAGTGTCCAGTCTGAAGTGGCCAGAGCCAGGA 715

RESULT 13
 BUI80020 945 bp mRNA linear EST 04-SEP-2002
 LOCUS BUI80020
 DEFINITION AGENCOURT_8106750 NIH_MGC_112 Homo sapiens CDNA clone IMAGE:6253787
 5', mRNA sequence.
 ACCESSION BUI80020
 VERSION BUI80020.1 GI:22694004
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 945)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (ULNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
 Plate: LNCM2402 row: d column: 12
 High quality sequence start: 13
 High quality sequence stop: 667.

REFERENCE
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (ULNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
 Plate: LNCM2402 row: d column: 12
 High quality sequence start: 13
 High quality sequence stop: 667.

FEATURES

source

1..945
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 /mol_type="mRNA"
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 /clone="IMAGE:6253787"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 3.53e-86 Length: 945
 Score: 1172.00 Matches: 214
 Percent Similarity: 99.5% Conservative: 0
 Best Local Similarity: 99.5% Mismatches: 1
 Query Match: 68.1% Indels: 1
 DB: 5 Gaps: 0

US-09-762-577B-12 (1-309) x BU180020 (1-945)

QY 1 MetGlyProLyAspSerAlaValysCysLeuHisArgGlyProGlnProSerHisTTPAla 20
 DB 90 ATGGAGCTTAAGACAGTGCAGAGTGCCTGCACCGTGAGCACAGCCGAGCCACTGGGCA 149
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 DB 150 GCCGGTGAATGTCCTCCACGAGAGAGCGCTGTGACCCCGCTCTCTGGGAGCCCTGTCTA 209
 QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 DB 210 GGCTTGGACACCTGACAGACCTGGGACCACTGGATGGGACATCTGGGCGAGCTGGCG 269
 QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 DB 270 CCCCTGACAG 329
 QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyAspTTPProLeuThr 100
 DB 330 TTCCCGGCGATGGGCTCTGAGAGATTCGCTCTGGCTCTCTTATGACTGGCCGCTGACT 389
 QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 DB 390 GGTGAGGTGCACCCGAGGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 449
 QY 121 LysValArgCysPhePheCysTyArgGlyLeuGlnInsertTTPLyAspArgGlyAspAspPro 140
 DB 450 AAGGTGAGGTGCTCTCTGCTATGAGGGGCTGACAGAGCTGGAACCGGGGAGACACACCC 509
 QY 141 TTPThrGlnHisAlaTyArgTTPPheProSerCysGlnPheLeuLeuArgSerLyAspGlyArg 160
 DB 510 TGGAGGAGGACATGCCAAGTGTCCCACTGTCTGCTGTCTGTCTGTCTGTCTGTCTGT 569
 QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
 DB 570 GACTTGTTCACAGTGTGACAGAGACTCACTCCAGCTGTGGCTCTGTGGGACCCGTGG 629
 QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyTTPProGln 200
 DB 630 GAAGAACCAG 689
 QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlu 215
 DB 690 CTGCCACCCCAAG-AGAGAGGTCCAGTCTGAAGGTGCCCAAGAA 733

RESULT 14

CD051153 891 bp mRNA linear EST 09-MAY-2003

LOCUS AGNCORRT_13976914 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.

DEFINITION AGNCORRT_13976914 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CD051153.1 GI:30488777

VERSION CD051153.1 GI:30488777

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 891)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgsbds-remail.nih.gov

Tissue Procurement: Dr. Jamie Thompson, University of WI

cDNA Library Preparation: Gina Zastrow-Hayes

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Identification: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDMK35 row: d column: 07
 High quality sequence start: 18
 High quality sequence stop: 718.

FEATURES

source

1. 891
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 /cissue_type="embryonic trophoblasts, made from WA01 stem
 cells"
 /lab_host="DH10B Tona"
 /clone_id="NIH_MGC_173"
 /note="vector: pDONR201; Site 1: atp2; Site 2: atp1;
 LIBR PRIMING - oligo dT; METHOD - full-length enriched;
 LIBR PROVIDER - Bradfield"

ORIGIN

Alignment Scores:

Pred. No.: 6.77e-85 Length: 891
 Score: 1156.00 Matches: 214
 Percent Similarity: 97.7% Conservative: 1
 Best Local Similarity: 97.3% Mismatches: 3
 Query Match: 67.2% Indels: 2
 DB: 6 Gaps: 0

US-09-762-577B-12 (1-309) x CD051153 (1-891)

QY 1 MetGlyProLyAspSerAlaValysCysLeuHisArgGlyProGlnProSerHisTTPAla 20
 DB 214 ATGGAGCTTAAGACAGTGCAGAGTGCCTGCACCGTGAGCACAGCCGAGCCACTGGGCA 273
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 DB 274 GCCGGTGAATGTCCTCCACGAGAGAGCGCTGTGACCCCGCTCTCTGGGAGCCCTGTCTA 333
 QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 DB 334 GGCTTGGACACCTGACAGAGCTGGGACCACTGGATGGGACAGATCTGGGCGAGCTGGCG 393
 QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 DB 394 CCCCTGACAG 453
 QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyAspTTPProLeuThr 100
 DB 454 TTCCCGGCGATGGGCTCTGAGAGTGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 513
 QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 DB 514 GCTGAGGTGCCACCGAGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 573
 QY 121 LysValArgCysPhePheCysTyArgGlyLeuGlnInsertTTPLyAspArgGlyAspAspPro 140
 DB 574 AAGGTGAGGTGCTCTCTGCTATGAGGGGCTGACAGAGCTAGAAAGCGGGGAGACGACCC 633
 QY 141 TTPThrGlnHisAlaTyArgTTPPheProSerCysGlnPheLeuLeuArgSerLyAspGlyArg 160
 DB 634 TGGAGGAGGACATGCCAAGTGTCCCACTGTGAGTTCCTGTCTGTCTGTCTGTCTGTCT 693
 QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
 DB 694 GACTTGTTCACAGTGTGACAGAGACTCACTCCAGCTGTGGCTCTTGGGACCCGTGG 753
 QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyTTPProGln 200
 DB 754 GAAGAACCAG 813
 QY 201 LeuProThrProArg-ArgGluValGlnSerGlnSerAla-GlnGluProGlyAla 218

DB	814	CGCCACACCCAGGAGAGGTCCAGTTCCTTGAAGTGCCTCCAGGACGATGCA	869
RESULT 15			
LOCUS	BO877652		
DEFINITION	BO877652	919 bp	mRNA
ACCESSION	AGNCOURT_8095636	NIH_MGC_112	Homo sapiens cDNA clone IMAGE:6087865
VERSION	BO877652		
KEYWORDS	BO877652.1	GI:22269660	EST.
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (Bases 1 to 919)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		

FEATURES	Location/Qualifiers
source	1. .919

ORIGIN

Alignment Scores:

Req. No.:	1.14e-84	Length:	919
Score:	1153.50	Matches:	233
Percent Similarity:	83.2%	Conservative:	6
Best Local Similarity:	81.1%	Mismatches:	21
Query Match:	67.0%	Indels:	28
DB:	5	Gaps:	4

US-09-162-577B-12 (1-309) x BQ877652 (1-919)

QY	1	MetGlyProLysAspSerAlaIysCysLeuHISargGlyProGlnProSerHisTyrPala	20
Ddb	64	ATGGACCTTAAAGACATGGCCAAAGTCCGTGCACCGTGGACCAAGCCGACCTGGGCA	122
QY	21	AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu	40
Ddb	124	GCCGGTGATGGTCCACGACGAGAGGGCTGTGACCCCGCTCTTGGGACGCCCTGTCTTA	183
QY	41	GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg	60
Ddb	184	GACCTGGACACCTGGACAGCCTGGGACCACTGGATGGGACAGATCTTGGGCGACACTGGG	243
QY	61	ProLeuThrGluGlnGluGlnGluGlyAlaGlyAlaThrLeuSerArgGlyProAla	80

[illegible]

Search completed: April 19, 2006, 21:22:57
Job time : 4518 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 19, 2006, 21:27:10 ; Search time 548 Seconds
(without alignments)
2281.754 Million cell updates/sec

Title: US-09-762-577b-12
Perfect score: 1721
Sequence: 1 MGRKDSAKCLHRGPQPSHMA.....GLQSGHAPLCLFWTFVWAC 309

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 928580 seqs, 2023302648 residues
Total number of hits satisfying chosen parameters: 18577160

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-O=/abse/ABSSMB.spool/US09762577/rnat_19042006_11113_25100/app_query.fasta.1
-DB=Published.Applications.NA.New -QFMT=fastcap -SUFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.cdt -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abse05h
-USRR=US09762577 @CCN 1.1 657 @rnat_19042006_11113_25100 -NCPV=6 -ICPV=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOCK -DEV TIMEOUT=120
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.New:*
1: /SIDS5/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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4: /SIDS5/ptodata/1/pubpna/PC1_NEW_PUB.seq:*
5: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
7: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
9: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
10: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
11: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1372.5	79.8	769	US-11-135-855-22	Sequence 22, Appl
2	1354	78.7	1068	US-11-135-855-21	Sequence 21, Appl

3	479	27.8	3837	14	US-11-136-527-2596	Sequence 2596, Ap
4	472	27.4	3076	7	US-10-960-414-432	Sequence 432, App
5	464	27.0	2106	14	US-11-136-527-2757	Sequence 2757, Ap
6	409	23.8	2468	14	US-11-136-527-303	Sequence 303, App
7	399	23.3	1575	14	US-11-102-026A-114	Sequence 114, App
8	297.5	17.2	1097	8	US-10-750-185-33882	Sequence 33882, A
9	297.5	16.3	1097	8	US-10-750-623-33882	Sequence 33882, A
10	278.5	16.2	600	8	US-10-750-623-33882	Sequence 33882, A
11	278.5	16.2	600	8	US-10-750-623-33882	Sequence 33882, A
12	255	14.8	5365	14	US-11-091-928-4	Sequence 21867, A
13	255	14.8	5984	14	US-11-091-928-3	Sequence 4, Appl1
14	241.5	14.0	600	14	US-11-136-527-6653	Sequence 3, Appl1
15	194.5	11.3	2136	11	US-11-072-512-618	Sequence 685, Ap
16	188.5	11.0	1507	8	US-10-750-185-21867	Sequence 618, App
17	188.5	11.0	1507	8	US-10-750-623-38201	Sequence 38201, A
18	179	10.4	660	6	US-09-925-065A-657778	Sequence 38201, A
19	173.5	10.1	2655	14	US-11-112-908-9	Sequence 657778, A
20	164.5	9.6	1793	11	US-11-096-568A-25627	Sequence 9, Appl1
21	160	9.3	1619	7	US-10-960-414-105	Sequence 25627, A
22	160	9.3	1619	8	US-10-947-249-108	Sequence 105, App
23	155.5	9.0	3151	11	US-11-072-512-602	Sequence 108, App
24	150	8.7	1615	11	US-11-096-568A-17561	Sequence 602, App
25	145.5	8.5	559	14	US-11-128-061-1885	Sequence 17561, A
26	145.5	8.5	559	14	US-11-128-061-5527	Sequence 1885, Ap
27	145.5	8.5	559	14	US-11-128-049-1885	Sequence 5527, Ap
28	145.5	8.5	559	14	US-11-128-049-5527	Sequence 1885, Ap
29	143	8.3	904	14	US-11-136-527-2655	Sequence 5527, Ap
30	143	8.3	904	14	US-11-136-527-6751	Sequence 2655, Ap
31	142.5	8.3	1651	11	US-11-096-568A-4646	Sequence 6751, Ap
32	139	8.1	5882	11	US-11-250-759-246	Sequence 4646, Ap
33	138	8.0	3072	11	US-11-250-759-246	Sequence 244, App
34	137	8.0	1536	11	US-11-096-568A-7753	Sequence 7753, App
35	136.5	7.9	1668	11	US-11-096-568A-21962	Sequence 71962, A
36	134	7.8	1632	11	US-11-096-568A-8213	Sequence 8213, Ap
37	134	7.7	1945	11	US-11-096-568A-10279	Sequence 10279, A
38	132.5	7.7	506	14	US-11-136-527-1014	Sequence 1014, Ap
39	132.5	7.7	506	14	US-11-136-527-5110	Sequence 5110, Ap
40	131.5	7.6	1831	11	US-11-096-568A-7679	Sequence 7679, Ap
41	131	7.6	2323	11	US-11-250-759-245	Sequence 245, App
42	131	7.6	4333	8	US-10-775-169-192	Sequence 192, App
43	129	7.5	1751	8	US-10-750-185-34107	Sequence 34107, A
44	129	7.5	1751	8	US-10-750-623-34107	Sequence 34107, A
45	129	7.5	2803	8	US-10-947-249-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-11-135-855-22
; Sequence 22, Application US/1135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-135-855-22

Alignment Scores:

Pred. No.: 4,25e-88 Length: 769
 Score: 1372.50 Matches: 255
 Percent Similarity: 91.1% Conservative: 0
 Best Local Similarity: 91.1% Mismatches: 1
 Query Match: 79.8% Indels: 25
 DB: 14 Gaps: 1

US-09-762-577B-12 (1-309) x US-11-135-855-22 (1-769)

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QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGAACCTTAAGACAGTGCACAGTGCCTGACACCTGACACAGCCGACCTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProAspSerLeuGlySerProValLeu 40
DB 61 GCCGGTGTATGTCCTCCACCGACGAGGCTGTGTGACCCGCTCTCTGGGCAAGCCCTGTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 121 GCCCTGACACCTGACAGACCTGGGACCACTGGATGGGACAGATCCTGGGCAAGCTCGG 180
QY 61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 241 TTCCCGGCGATGGGCTCTGAGAGAGTGTGGTCTGAGCTCTCTCTATATGACTGGCCGCTGACT 300
QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTAAGGTGACACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 360
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 361 AAGGTGAGGTGCTCTCTCTGCTATGGGGGCTGTGAGAGCTGTGAGAGAGAGAGAGAGAGAG 420
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 421 TGGACGAGAGATGCTCAAGTGTGCTCCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 478
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
DB 479 GACTTGTCCACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 538
QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 539 GAAGAAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 574
QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGluAlaArgAsp 220
DB 575 -----GAGACCAAGGAT 586
QY 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
DB 587 GTGAGAGCGGAGCTGTGGGGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 646
QY 241 AlaValSerTrpLysValPheValProCysGlyHisLysLeuValCysAlaGlnCysAlaProGly 260
DB 647 GCCGTGTTCATCCTCTTGTGTGTGCGGGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 706
QY 261 LeuGlnLeuCysProTrpLysArgAlaProValArgSerArgValArgThrPheLeuSer 280
DB 707 CTGCAAGCTGTGCCCCATCTGTGCAAGAGCCCGGTCCGAGCGGCGGACCACTTCTGTCTC 766

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RESULT 2
 US-11-135-855-21

/ Sequence 21, Application US/1135855
 / Publication No. US2005025557A1
 / GENERAL INFORMATION:
 / APPLICANT: SMITHKLINE BEECHAM CORPORATION

```

/ APPLICANT: SMITHKLINE BEECHAM P.L.C.
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50013
/ CURRENT APPLICATION NUMBER: US/11/135,855
/ CURRENT FILING DATE: 2005-05-24
/ PRIOR APPLICATION NUMBER: US/10/203,708
/ PRIOR FILING DATE: 2002-08-13
/ PRIOR APPLICATION NUMBER: PCT/US01/04703
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: 60/182,172
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: 60/186,084
/ PRIOR FILING DATE: 2000-02-29
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 21
/ LENGTH: 1068
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-135-855-21

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Alignment Scores:

Pred. No.: 1.17e-86 Length: 1068
 Score: 1354.00 Matches: 267
 Percent Similarity: 76.4% Conservative: 5
 Best Local Similarity: 75.0% Mismatches: 8
 Query Match: 78.7% Indels: 77
 DB: 14 Gaps: 5

US-09-762-577B-12 (1-309) x US-11-135-855-21 (1-1068)

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QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGAACCTTAAGACAGTGCACAGTGCCTGACACCTGACACAGCCGACCTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProAspSerLeuGlySerProValLeu 40
DB 61 GCCGGTGTATGTCCTCCACCGACGAGGCTGTGTGACCCGCTCTCTGGGCAAGCCCTGTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 121 GCCCTGACACCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 421 TGGACGAGAGATGCTCAAGTGTGCTCCCACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 177
DB 481 GACTTGTCCACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 177 ----- 177
DB 541 ACCTTCTCGGGGCTCGGGTGTGAGTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 600
QY 178 -----AspProTrpGlnGluProGluAspAlaAlaProValAla 190

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Db 601 GATGCTCTGCGCTCTTCCAGAACCCGTGGAAAGAACCGGAGACGACGCCCTGTGGC 660
 Qy 190 aProSerValPro----- 194
 Db 661 CCCCTCCGCGTCCAGTCTGAAGTGCCAGAGCCAGTGCGAGCCCGGAGACCCCTGTGGT 720
 Qy 195 -----AlaSerGlyTyrProGluLeuProThrPro----- 204
 Db 721 GAGGCTGGGAGGAGGAGGAGGAGGAGGAGC-CCGACCTTCATGAGCCCATAGAGGAGTG 779
 Qy 205 -----ArgArgGluVal-----G1 209
 Db 780 GGGCCAGGGGTGGGAGCAATTTCCAGAGCTGTCTCTTACGAGGGGTCACTCCAGCCGA 839
 Qy 209 nSerGluSerAla-----GlnGluProGluValAlaArgSerValGluAlaGlnLe 225
 Db 840 GGGCCAGAGGGCGCGTGGGCTTTTGAAGCCCCCAGAGCCAGGAGTGTGAGGGCGAGCT 899
 Qy 225 uArgArgLeuGlnGluArgThrCysValCysLeuAspArgAlaValSerIleVal 245
 Db 900 GCGGCGGCTGCAGAGGAGAGAGACGTGCAAGGTGTGCTGGACCGCGCGTGTCACTGT 959
 Qy 245 lPheValProCysArgIleHisLeuValCysAlaGluCysAlaProGlyLeuGlnLeuCysPr 265
 Db 960 CTTGTGCTCCGTGCGGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1019
 Qy 265 oileCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 Db 1020 CATCTGCAGAGCCCGCTCCGAGCCGCGTGGCACTTCTGTTC 1065

RESULT 3

US-11-136-527-2596
 ; Sequence 2596, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mount, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; PRIORITY FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2596
 ; LENGTH: 3837
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (3825)..(3831)
 ; OTHER INFORMATION: n is a, c, g, or t
 US-11-136-527-2596

Alignment Scores:
 Pred. No.: 2,77e-24 Length: 3837
 Score: 479.00 Matches: 122
 Percent Similarity: 35.6% Conservative: 33
 Best Local Similarity: 28.0% Mismatches: 93
 Query Match: 27.8% Indels: 188
 DB: 14 Gaps: 9

US-09-762-577b-12 (1-309) x US-11-136-527-2596 (1-3837)
 Qy 2 G1yProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTPrAlaAla 21
 Db 1567 GGGGCTGAGAGACAGGAGTGGCTGTTTGGCTGTGTGAGAACTGAGCACTGGAAACCG 1626
 Qy 22 G1yAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeuGly 41
 Db 1627 AACGATATCTTCTGTGAGAGCAC----- 1650

Qy 42 LeuAspThrCysAlaGalaTPrAspHisValAspGlyGlnIleLeuGlnLeuArgPro 61
 Db 1651 -----AGGAGACATTTTCCCACTGT-----CCA 1674
 Qy 62 LeuThrGlu-----GluGluGluGluGluGlyValAlaGlyAlaThrLeuSerArgGlyPro 79
 Db 1675 TTTCTGAAAATACCTTCAGAAACGAGAGGTTTAGTATCAATCTCACT----- 1725
 Qy 80 AlaPheProGlyLeuGlySerGluGluLeuArgLeuAspPheTyrAspTrpProLeu 99
 Db 1726 -----ATGCAGACACACTCTGCTCGATGAGKACGTTTCTGTACTGGCCATCG 1773
 Qy 100 ThrAlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlnHisGln 119
 Db 1774 AGTGTCTTGTTCAGCTTCAGAGCTTCGAAAGTGCTGAGTTTATTATGTGATCAACAAT 1833
 Qy 120 AspLysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspArg 139
 Db 1834 GATGATGTCAAAATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1893
 Qy 140 ProThrThrGlnHisAlaLysTrpPheProSerCysGlyPheLeuLeuAspSerLysGly 159
 Db 1894 CTTGATATGACATGCGCAATGATGTTCCAGGTGTGAGTTTGTATACGATGAAAGGCT 1953
 Qy 160 ArgAspPheValHisSerValGlnGluThrHis-----SerGlnLeuLeuGly 175
 Db 1954 CAGAGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2013
 Qy 176 SerTrpAspProTrpGluProGluAspAlaAlaProValAlaProSerValProAla 195
 Db 2014 ACTTCAGACACCTTCAGAAAGAAATGCTGACCTTCAGATGTGTGATCTGGCCCTGGA 2073
 Qy 196 SerGlyTyrProGlu-----LeuProThrPro----- 204
 Db 2074 GAGAAATTGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2133
 Qy 204 ----- 204
 Db 2134 GCGTTCAGTAGAGCCGTGTGAGACAGAGGTTCAAGACAGATCTCGGCACTGGTAGAG 2193
 Qy 205 -----ArgArg 206
 Db 2194 AACTAGAGACGCTCAGTATATTTGTGAGCACTTCTGATGCTGAGATGAGAGAGA 2253
 Qy 207 GluValGlnSerGlySerAlaGlnGluProGlyAlaArg----- 219
 Db 2254 GAAGAGAGAGAGAGAGACAGTGAAGAGACGCGCATCAGTGACTTGTCAATTGATTCGG 2313
 Qy 219 ----- 219
 Db 2314 AAGAAATGAAATGAGCCCTCTTCCAAAGTGAAGTGTGTCTTCTTCTCGATGATCTT 2373
 Qy 219 ----- 219
 Db 2374 CTTGAGGCCAGTGTACTTACAAAGAGAGAAATGATATTATCAGACAGAAACACAGATA 2433
 Qy 219 ----- 219
 Db 2434 CCTTACAAAGAGAGAGACTCATGACACCACTTTAGTCAAGGAAATGCTGAGCAGC 2493
 Qy 219 ----- 219
 Db 2494 GTCTTAAAAACCTCTGAAAGAGATCGACTACGCTATATGACACATTTATTTGTGGAG 2553
 Qy 220 -----AspValGluAlaGlnLeu 225
 Db 2554 AAGACGATGAAGTATTTCCACAGAAAGCGTTTCAGGCTTGTCAATTGAGAAAGACAGCTG 2613
 Qy 226 ArgArgLeuGlnGluGluArgThrCysLysValCysLeuAspArgAlaValSerIleVal 245
 Db 2614 CGGAGATTACAAAGAAAGAAAGCGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2673
 Qy 246 PheValProCysGlyHisLeu-----ValCysAlaGluCysAlaProGlyLeuGlnLeuCys 264

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Db      2674 TTGATTCCTGTGTCATCTGTCAGTCCCGGAATGAGCCCTTCCTGAGAAAGTGC 2733
QY      265  ProileCyArGAlaProValArGserArGValArGThrPheLeuSer 280
Db      2734 CCATCTGACGGGGGACATTAAGGAGCTGTGCGTAGCTTCTCTCA 2781

RESULT 4
US-10-960-414-432
/ Sequence 432, Application US/10960414
/ Publication No. US2006007456A1
/ GENERAL INFORMATION:
/ APPLICANT: MILLER, LANCE D.
/ APPLICANT: GEORGE, JOSH
/ APPLICANT: VEGA, VINCENTIUS B.
/ TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
/ FILE REFERENCE: 38271-76067
/ CURRENT APPLICATION NUMBER: US/10/960,414
/ NUMBER OF SEQ ID NOS: 500
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 432
/ LENGTH: 3076
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-960-414-432

Alignment Scores:
Pred. No.: 7,08e-24 Length: 3076
Score: 472.00 Matches: 118
Percent Similarity: 37.7% Conservative: 47
Best Local Similarity: 26.9% Mismatches: 85
Query Match: 27.4% Indels: 188
DB: Gaps: 11

US-09-762-577b-12 (1-309) x US-10-960-414-432 (1-3076)
QY      1  MetGlyProLyAspSerAlaLysCyLeuHiAArgGlyProGlnProSerHiStrPaLa 20
Db      1313 ATAGAGACCTGGAGACAGAGTGGCTTGGCTTGGCTGTCGAGAAATTAAGCAATGGGA 1372
QY      21  AlaGlyAspGlyProThrGlnGlu-----ArgCysGlyProArGserLeuGlySerPro 38
Db      1373 CCGAAGGATATAGTGTATGTATGTACAGACCTGAGACATTTCCCAA----- 1417
QY      39  ValLeuGlyLeuAspThrCyArGAlaATrPArPHisValAspGlyGlnLeuGlyGln 58
Db      1418 -----TGC----- 1420
QY      59  LeuArGProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 78
Db      1421 -----CCATTATAGAAATTCAGCTTCAAGACACTTCAAGATTAACAGATTCTATAT-- 1471
QY      79  ProAlaPheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 98
Db      1472 -----CTGACATGACGACACATGACGCCCGCTTTAAACATCTTTAACTGGCCC 1522
QY      99  LeuThrAlaGlnValAlaProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHis 118
Db      1523 TCTAGGTTCTAGTATATCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 1582
QY      119  GlnAspLysValArGAspPhePheCysPheCysPheCysPheCysPheCysPheCysPhe 138
Db      1583 AGTGATGATGTCAAAATGCTTTGCTGTATGTATGTATGTATGTATGTATGTATGTATGTAT 1642
QY      139  AspProThrThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArGserLys 158
Db      1643 GATCCATGGGTTCAACATGCCCAAGTGTTCCTCAAGGTGTGATGATGATGATGATGATGAT 1702
QY      159  GlyArGAspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySer----- 176
Db      1703 GGAAGAGAGTTATATCCGTCAAGTTCAAGCCAGTAACTCTATCTTAAGTAACTGCTGTA 1762

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QY      177 -----TrpAspPro 179
Db      1763 TCCACATCAGACAGACCCAGAGATGAAATATGAGAGTCAATTAATTCATTAAGTCACT 1822
QY      180  TrpGlnGlu---ProGlnSerAla-----AlaProValAlaProSerValPro 194
Db      1823 GGAAGAGACCATTCAGAAAGATGCAATCATGATGATGATGATGATGATGATGATGATGATG 1882
QY      195  AlaSerGlyTyPProGlu-----LeuProThr 203
Db      1883 GAAATGGCTTATAGTGAAGCCTGGTAAACAGACAGTTCAAAAGAAAATCTTACCAACT 1942
QY      204  Pro----- 204
Db      1943 GAGAGAAATTAATAGACTAGTCAATGATCTGTGTAGACTTACTCATGACAGAAATGAA 2002
QY      205  ---ArgArGlnValGlnSerGlnSerAlaGlnGlnUpProGlyAlaArGAsp----- 220
Db      2003 ATTAGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2062
QY      220 ----- 220
Db      2063 ATCCGGAAGATTAAGATGACACTTTTCAAGATTGACTTGTATTCATTCCTGGAT 2122
QY      220 ----- 220
Db      2123 AGTCTACTAAGTCCGGAATTATTAATGACAGAGATGATGATTAATAACAGAGACA 2182
QY      220 ----- 220
Db      2183 CAGAGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2242
QY      220 ----- 220
Db      2243 GCCACTGATTCAAGAACTCTCTGCAAGAGCTGAGAGCTGTATATAGACATTTATTT 2302
QY      221 -----ValGlnAla 223
Db      2303 GTGCAACAGACATTAATATATATCCACAGAAAGATTTTCAGATTCACAGTGGAGAA 2362
QY      224  GlnLeuArGArGLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 243
Db      2363 CAATTGGGGAGACTCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2422
QY      244  IleValPheValProCysGlyHisLeu---ValCysAlaGlnCysAlaProGlyLeuGln 262
Db      2423 ATAGTGTATATCTCTGTGTGTATCATAGTATGCAAGAGATGCTCTCTCTTTAAGA 2482
QY      263  LeuCyAspProIleCyArGAlaProValArGSerArGValArGThrPheLeuSer 280
Db      2483 AAGTGTCTATTTTGTAGAGATACATCAAGGATGACAGTTCGATCTTCTTCA 2536

RESULT 5
US-11-136-527-2757
/ Sequence 2757, Application US/11136527
/ Publication No. US20050287570A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounes, William M
/ TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
/ FILE REFERENCE: 031896-04100 (AM101086)
/ CURRENT APPLICATION NUMBER: US/11/136,527
/ PRIOR FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US 60/574,294
/ NUMBER OF SEQ ID NOS: 362830
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2757
/ LENGTH: 2106
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-11-136-527-2757

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Alignment Scores:

Pred. No.: 1,84e-23 Length: 2106
 Score: 464.00 Matches: 122
 Percent Similarity: 37.2% Conservative: 40
 Best Local Similarity: 28.0% Mismatches: 86
 Query Match: 27.0% Indels: 188
 Gaps: 12

US-09-762-577b-12 (1-309) x US-11-136-527-2757 (1-2106)

QY 2 G1YProlysaAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTTPAlaAla 21
 DB 592 GGGCTCGGAATAGATAGTGGCTGCTTGGCTGGTGGTAACTGAACCACTGGAGATGT 651
 QY 22 G1YAspGlyProThrGlnGlu-----ArgCysGlyProArgSerLeuGlySerProVal 39
 DB 652 AAGGATATCTCTCTGTCAAGACAGACAGACATTCTCC----- 690
 QY 40 LeuG1YLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeu 59
 DB 691 -----ACTGCCCATTTCTTAAGATGTG---GGTCAGTTCACCTCAACATAC 735
 QY 60 ArgProLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 79
 DB 736 -----ACTGCTCTAAC----- 747
 QY 80 AlaPheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyraPTrpProLeu 99
 DB 748 -----CTAGACATGACAGACCCAGCAGCAGCAGTGTGTGAACGTTCTTACCTGGCTTCT 801
 QY 100 ThrAlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGln 119
 DB 802 AGGCTCTCGTTCATCTCTCAAGAACTTGCAAGTGGGGCTTTTATTCACGGAGACAGT 861
 QY 120 AspIlyValArgCysPhePheCysTyrglyGlyLeuGlnSerTyrAspGlyAspAsp 139
 DB 862 GATGACCTCAAGTCTTTGCTGTGATGTGGCTAAGATGCTGGAAATCGAGAGACAGC 921
 QY 140 ProTThrGluHisAlaLysTTPPheProSerCysGlnPheLeuAlaGlySerIlyGly 159
 DB 922 CCCGGGTGGAACCGCCCAAGTGTGTTCCAAGGTGTGAGTACCTTGATCAGAAATCCAAAGGC 981
 QY 160 ArgAspPheValHisSerValGlnGluThHisSerGlnLeu----- 173
 DB 982 CAAGAGTTCGTTGGCCCAAGTTCAAGCTGTGTTACCTCATCYACWKARASGCTRTATCT 1041
 QY 174 -----LeuGlySerTTP 177
 DB 1042 AVTTSRGRCTSSMSAGAMTSAGRSTSRAGAGGACGACRATTTGTCATGTGGGCCCTGGA 1101
 QY 178 AspProTTPGlu----- 181
 DB 1102 GAGAAATTTGGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1161
 QY 181 ----- 181
 DB 1162 GGTTCAGTAGAGCCTGTGTGAGACAGACGTTTCAGGRCAGATCTTGCCACTGTGAG 1221
 QY 181 ----- 181
 DB 1222 AACTACAGACGGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1281
 QY 182 -----GluProGluAspAla----- 186
 DB 1282 GAGAGACAGACGAGACAGAGCGGAGAGAGAGAGAGATGATGATGATGATGATGATGATG 1341
 QY 187 -----AlaProValAlaPro----- 191
 DB 1342 AAGAACAAATGTGCTTTCAACATTTGACGCTGTGACACCAATCCGTGATGCTC 1401
 QY 191 ----- 191

DB 1402 CTAAGTCCAGGCTCATTTACCGAAGAGAGTACAGATCCGTAAACAGAAACACACACACC 1461
 QY 192 -----SerValProAlaSerGly----- 197
 DB 1462 TTGACGGAAGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1521
 QY 198 -----TyrProGluLeuProThrProArg 205
 DB 1522 TTCAGAACTCCCTGCAGAAATCGAACCTCGGTTGTACAGATATTA---TTTGTCCGA 1578
 QY 206 ArgGluValGlnSerGluSerAlaGlnGluProGlyAlaArgAspValGluAlaGlnLeu 225
 DB 1579 CAGAACATTAGAGTCTTCCACAGATGACATTGACGCTTACCGATGGAAGAACAGTTG 1638
 QY 226 ArgArgLeuGlnGluGluArgThrCysIlyValCysLeuAspArgAlaValSerIleVal 245
 DB 1639 CGAAACTCCAGAGAGAGAGACGTGTAAAGTGTGTGAGACGAGAGAGTCCCTCTGTG 1698
 QY 246 PheValProCysGlyHis---LeuValCysAlaGluCysAlaProGlyLeuGlnLeuCys 264
 DB 1699 TTCATTCCCTGTGCGCATTTGCTGTGTGCAAGAAATGTGCCCCCTCTCTGAGAGAGTCT 1758
 QY 265 ProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 DB 1759 CCCATCTGCAGAGAGATATCAAGGACACAGTGCAGACATTTCTCTCC 1806
 RESULT 6
 US-11-136-527-303/C
 ; Sequence 303, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; PRIOR FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 303
 ; LENGTH: 2468
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-11-136-527-303

Alignment Scores:
 Pred. No.: 1.65e-19 Length: 2468
 Score: 409.00 Matches: 109
 Percent Similarity: 42.1% Conservative: 42
 Best Local Similarity: 30.4% Mismatches: 110
 Query Match: 23.8% Indels: 98
 Gaps: 16

US-09-762-577b-12 (1-309) x US-11-136-527-303 (1-2468)

QY 3 ProlysaAspSerAlaLysCysLeuHisArgGlyProGlnProSer-----HisTTPAla 20
 DB 1677 CCGAGAACCCGCGCCATGTGTGTGTAAGAACGACGACGTAAGACGTTTCAGAACTGG--- 1621
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 DB 1620 -----CCAGACTATGCCCATTTAAAGCCCAAGAGATTAGCTAGTGTGAGACTC 1573
 QY 41 -----GlyLeuAsp----- 43
 DB 1572 TACTACACGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1513
 QY 44 -----ThrCys---ArgAlaTTPAsp-----HisValAspGly-----Gln 54
 DB 1512 TGGAAACCTGTGACCGTGTGTCAGAGACAGAGACACTTTCCAACTGCTTCTTC 1453


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Db      1521 TTATACCAAGCGGCAATTCCGACCATGCTTTGCTGATATCTCTTCGACTGGCCAC 1580
Oy      304 --ThrValPheTyrAla 308
        ||| ||| ||| |||
Db      1581 GGACCACCTTGCTGGGCT 1597

RESULT 13
US-11-091-928-3
; Sequence 3, Application US/11091928
; Publication No. US20050261306A1
; GENERAL INFORMATION:
; APPLICANT: JOH-E, IKEDA
; TITLE OF INVENTION: Anti-neurodegenerative agents
; FILE REFERENCE: K7-A0501P-US(CIP)
; CURRENT APPLICATION NUMBER: US/11/091,928
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP2002-286400
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 5984
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-091-928-3

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Alignment Scores:	
Pred. No.:	2,876-08
Score:	255.00
Percent Similarity:	37.1%
Best Local Similarity:	27.8%
Query Match:	14.8%
DB:	14
	Gaps: 20
US-09-762-577B-12 (1-309) x US-11-091-928-3 (1-5984)	

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Oy 11 HLAARGSLYProglInProSerHis-----TPRLAALAGLYAserylProthcIn 27
Db 630 CATMAAAGCCACCAAGAGGTTTCATCCAGATTGTGGGTT-----CCTTTTGA 677b
Oy 28 GLUATGCGSLYProArgSerLeuGlySerProValLeuGlyLeuAspThrCysArgAla 47
Db 678 CAAGAGTGT----- 666b
Oy 48 TPAPRHSValAspSLYGLInIleLeuGlyGLInLeuArgProLeuThrGLUGLUGLU 67
Db 687 TGGTAACATTGC-----CAAGTACGACATPAAGGGTGAAGAAATCTGAA 728
Oy 68 GLUGLUGLY-ALAGLYAlaThrLeuSerArgGLYProAlaPheProGLYMetGLYSerGL 87
Db 729 GAGCAGGCGTGAAGAGAGTAAATATGAG-----TACCAAGAGA 767
Oy 87 uGLuLeuArgPLeuAlaSerPheTyraSPTrpProLeuThraGLU---ValProProGL 106
Db 768 GGAAGCGTAAAGCTTGACATCTTCACAGAACTGGCCATTTATGTCACAGGAATATCCCTTC 827
Oy 106 uLeuLeuAlaAlaAGLYPhePheHisThrGLYHisGLInAspLYsValArgCysPhePh 126
Db 828 TGTCCTCTCCAGAGCTGGCTTGTCTTTCACAGTAAACAGACACCGGACAGTGTTTTTC 887
Oy 126 eCySLYGLYGLYLeuGlnSerTrpLYsArgLYsAspProTrpPhrGLYHisAlaLY 146
Db 888 CTGTGGTGGAGATGTTTNGAAATATGGGAAGAAGAAATATATCTCTGGAAGAACATGCGCA 947
Oy 146 sTrpPheProSerCysGLInPheLeuLeuArgSerLYsGLYArgAsp-----Ph 162
Db 948 ATGGTATCCCAAAATGTGAATTTCTTCGAGTAAAGAAATCCCAAGAGAAATTAACCCAGTA 100b
Oy 162 eValHisSer-----ValGLInIuThrHisSerInLeuGlySerTrpAs 178
Db 1008 TATTCAAAGCTACAGAGGATTTGTTCACACTAAGCGGAAGAACATTTTGTGAATTCCTGGGT 1067
Oy 178 pProTrpGLUGLUProGLInAspAlaAlaProValAlaProSerValProAlaSerGLY 198

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Db 1068 CCAAGAGAAATTACCTATGGCAATGGCACTTATTTGCAATGACAGCACTTTGCT-----TA 1122
QY 198 rProgluLeu-----ProThrProArgArgIuValGlnSerGluse 212
Db 1122 CGAAGAACTACGCGTGAAGCTTTTAAAGCATGCGCCCGGGAATCAGCTGTGGAGTTGC 1182
QY 212 rAlaGlnIuLeu-----ProGluAlaArgPvalIGluAlaGlnLeuArg 226
Db 1182 AGACACTGGCCAAAGCAGAGCTTTTCTTACACAGGTATTTAAAGGCATCTGCCAGTCTTT- 1239
QY 226 gArgLeuGlnGlnIuArgThrCysIysValCysLeuAspArg----- 240
Db 1240 -----TCTCTGGAGAGGGTTTAAAGAAATGCCAGAAAGTGATGA 1280
QY 241 -----AlaValSerIleValPheValProCysGluIleLeu-----Va 253
Db 1281 CCCATTAGACGATCACACCCAGATGTTTTCCCAATTTGTCATTCTCCAAATATGAATGC 1340
QY 253 lCysAlaGluCysAlaProGluLeuGln-----LeuCysProIleCysArgAl 269
Db 1341 CTCTGGCGAAGTACCTCCAGACCTTCAAGCCCGTGTGAATCTTTGTGAATTACTGGAAC 1400
QY 269 aProValArgSerArgValArgThrPheLeuSer-----**AlaArgCy 284
Db 1401 CACAAGTGAAGACCATCTTGAAGATTCAATAGCAGTTGCTCTATAGGCCAGAAATGCG 1460
QY 284 sHisGly-ArgProGluIleLeu-----GlnSerG 294
Db 1461 AAGAGGTGAAGCCAGTGTGTTCAAGAGCCAAAGAAATCTGAATGACGAGCTGAGAGCGC 1520
QY 294 lYLeuProAlaPro-----LeuCysIleu-----PheTyr--- 303
Db 1521 TTATACCGACGCGCAGTTTCCGCAACATGCTTTTCTTGATATCTCTCCATCTGGCAC 1580
QY 304 --ThrValPheTyrAla 308
Db 1581 GGACCACTTGCTGGGCT 1597

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RESULT 14
US-11-136-527-6853
; Sequence 6853, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ. ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6853
;
; LENGTH: 600
;
; TYPE: DNA
;
; ORGANISM: Rattus norvegicus
US-11-136-527-6853

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Alignment Scores:
Pred. No.:      3.14e-08
Score:          241.50
Percent Similarity: 74.0%
Best Local Similarity: 57.1%
Query Match:    14.0%
DB:             14
Gaps:           1

US-09-762-577B-12 (1-309) x US-11-136-527-6853 (1-600)

OY      205  ArgArgGlValaGlnSerCluSerAlaGlnGluPProGlyAlaArgAepValGluValaGln 224
Db      :      :      :      :      :      :      :      :      :      :
       70  CGACACAACTATGAGAGTCTTCCACACAGATATACATGTGAGCTTCACCGATGGAAAGACAG 129

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Qy 225 LeuArgArgLeuGlnGluArgThrCysLeuAspArgAlaValSerIle 244
Db 130 TTGGGAACCTCCAGAGAGAGAACTGTAAAGTGTATGACACGAGAGTCTC 189
Qy 245 ValIheValProCysGlyHis--LeuValCysAlaGluCysAlaProGlyLeuGlnLeu 263
Db 190 GTGTTCAATTCCTCTGGCCATMTGTGCTGTGCAAGAAATGTGCCCCCTCTGTAGAAAG 249
Qy 264 CysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 250 TGTCCCATCTGCAAGAGGATATCAAGGGCAAGTGGCGCACATTTCTCTCC 300

RESULT 15
US-11-072-512-618
; Sequence 618, Application US//11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: MAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAOBU
; APPLICANT: MAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US//11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 618
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-618

Alignment Scores:
Pred. No.: 0.000211 Length: 2136
Score: 194.50 Matches: 79
Percent Similarity: 35.6% Conservative: 33
Best Local Similarity: 25.1% Mismatches: 98
Query Match: 11.3% Indels: 105
DB: 11 Gaps: 13

US-09-762-577b-12 (1-309) x US-11-072-512-618 (1-2136)
Qy 12 ArgGlyProGlnProSerHisThrAlaAla----- 21
Db 1293 AGGGGGACACAGCCCTGCAAGTGGCGCTGCAAGCTCATCAAGCTGCTGCCCTGTGGCTG 1352
Qy 22 ---GlyAspGlyProThrGlnGluArgCys-----GlyProArgSerLeuGly 36
Db 1353 ATGGGGCGGGGGGGAGACCGAGGCGCTGTGACAGCTGCTGCAAGCTCAAGGCTCGGGCC 1412
Qy 37 SerProValLeu-GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLe 56
Db 1413 TCCCGGCGACGCGGAGACTGACGGTGGCGCGGC-----GGTGGCTGTGCT 1457

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Qy 56 u-----GlyGlnLeuArgProLeuThrGlnGluGlnGluGlnGluGln 72
Db 1458 TCTCGGGCTGGAGAGGGCGCGAGCTGAGCTACACCAACACCGGGCTGCGAGCCGCTGG 1517
Qy 72 Y-----AlaThrLeuSerArgGly-----ProAlaPheProG 83
Db 1518 ACCTGGCGCGCGAGAGGTGCGGTGCTCAAGGCGCTTCAAGGGCTGGCGCCAGCGCTCGGG 1577
Qy 83 yMetGly-----SerGlnGluLeuArgLeuAlaSerPhe 94
Db 1578 AGCGGACGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1637
Qy 94 eTyRAspTrpProLeuThrAlaGlu-----ValProProG 106
Db 1638 CCGTGAAGAACTGTCACAGTGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGT 1697
Qy 106 uLeuLeuAlaAlaGly-PhePheHisThrGlnHisGlnAspGlyValArgCysPheP 126
Db 1698 GCTCCGAGCTGGCGCTGCTGTGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1757
Qy 126 heCysTyrglyGlyLeuGlnSerTrpIleArgGlyAspAspProTrpThrGlnHisAla 146
Db 1758 AGTGGCGCGCGAGATGAAAGATGCAATCAG----- 1789
Qy 146 ystTrpPheProSerCysGlnPheLeuLeuArgSerIleGlyArgAspPheValHisSerV 166
Db 1790 -----TGCAGGTGTGTGTCAAGAAACTGCGC----- 1819
Qy 166 aGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrpGlnGluProGlnAspA 186
Db 1820 -----CCAGACG 1826
Qy 186 laAlaProValAlaProSerValProAlaSerGlyTrpProGlnLeuProThrProArgA 206
Db 1827 GCTCTGAGTGGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1871
Qy 206 rgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAspValGlnAlaGlnLeuA 226
Db 1872 AGCTGTGGAG-----GAGCTGGAGAGCGGCTACG 1901
Qy 226 rgArgLeuGlnGlnGluArgThrCysLeuValCysLeuAspArgAlaValSerIleValP 246
Db 1902 GGCAGATGAGAGAACCATCAGCTGCCCATCTGATCGACAGCCATCGGCTGTGT 1961
Qy 246 heValProCysGlyHisLeuValCysAlaGluCysAlaProGlyLeuGlnLeuCysProI 266
Db 1962 TC---CAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 2018
Qy 266 leCysArgAlaProValArgSerArgValArgThrPheLeu 279
Db 2019 TCTGGCGCGAGCCCATCGGACCGGATCCAGATCTTCGTG 2059

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Search completed: April 19, 2006, 21:51.18
Job time : 561 secs

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